

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 03:48:54 ; Search time 2617 Seconds  
(without alignments)  
14283.192 Million cell updates/sec

Title: US-10-727-010-1

Perfect score: 982  
Sequence: 1 CGGCCGATCACCACATCTCCG.....TCGGCTCTCTGAGTAAAC 982

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsa1:\*  
9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	129.2	13.2	1910	AG382199	Mus muscu
C 2	127.6	13.0	1297	CG744520	P037-1-EI
C 3	127	12.9	1277	CG753585	P048-3-HI
C 4	126.6	12.9	1601	CG752479	P047-2-AO
C 5	126	12.8	1565	AG340866	Mus muscu
C 6	126	12.8	1567	CG746709	P040-1-B0
C 7	125.6	12.8	1695	CC290874	CH261-172
C 8	125.4	12.8	1874	AG448338	Mus muscu
C 9	125	12.7	2041	AG363808	Mus muscu
C 10	124.4	12.7	1107	CK162505	FCAS01510
C 11	124.4	12.7	1193	AG349830	Mus muscu
C 12	124	12.6	1471	CG748176	P042-1-A0
C 13	124	12.6	1616	CG753270	P048-2-C0
C 14	123.2	12.5	1970	CG748837	P042-4-E0
C 15	123	12.5	1087	CB908860	tr1c074xf
C 16	123	12.5	1087	CF882340	tr1c086xi
C 17	122.8	12.5	1836	AG382181	Mus muscu
C 18	122	12.4	1738	CG750956	P045-2-H0
C 19	121.6	12.4	1448	CC220110	CH261-92F
C 20	121.2	12.3	1082	CC300639	CH261-66F
C 21	121.2	12.3	1106	CB905422	tr1c074xf
C 22	121.2	12.3	1106	CF876941	tr1c074xf
C 23	121.2	12.3	1223	AG441637	Mus muscu
C 24	121.2	12.3	1258	AG441605	Mus muscu

C 25	121.2	12.3	1397	CL105166	ISB1-44E1
C 26	121.2	12.3	1400	AG429585	Mus muscu
C 27	120.8	12.3	1093	CB905750	tr1c075xp
C 28	120.8	12.3	1093	CF877401	tr1c075xp
C 29	120.8	12.3	1642	CG754720	P050-2-A0
C 30	120.6	12.3	1249	CB905420	tr1c074xf
C 31	120.6	12.3	1249	CF876940	tr1c074xf
C 32	120.6	12.3	1961	AG435522	Mus muscu
C 33	120.4	12.3	1385	CL044197	CH216-60G
C 34	120.2	12.2	1011	CB905602	tr1c075xf
C 35	120.2	12.2	1011	CF877292	tr1c075xf
C 36	120	12.2	1314	CG748456	P042-2-D1
C 37	120	12.2	1506	AG442117	Mus muscu
C 38	119.8	12.2	1307	CL647465	CH213-139
C 39	119.8	12.2	1839	CG747711	P041-2-B0
C 40	119.6	12.2	1204	CC284084	CH261-167
C 41	119.4	12.2	1008	AG395157	Mus muscu
C 42	119.4	12.2	1491	CG748472	P042-2-E0
C 43	119.2	12.1	1151	CB905418	tr1c074xf
C 44	119.2	12.1	1151	CF876938	tr1c074xf
C 45	119.2	12.1	1197	BI416470	hasp001xa

## ALIGNMENTS

RESULT 1  
LOCUS AG382199/c 1910 bp DNA linear GSS 03-JUN-2004  
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-192123.T7, genomic survey sequence.  
ACCESSION AG382199  
VERSION AG382199.1 GI:47993404  
KEYWORDS GSS.  
SOURCE Mus musculus molossinus  
ORGANISM Mus musculus molossinus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1  
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
BAC end Sequences of Library MSMg01  
Unpublished  
2 (bases 1 to 1910)  
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan  
1-7-22 Suehiro-chou, Tsukuba, Ibaraki, Japan, 305-0074 Japan  
Tel: 81-45-503-9111, Fax: 81-45-503-9170  
E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/  
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kunita Abe (abe@tc.riken.jp).  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Tsukuba Institute, Bio Resource Center,  
Koyadai, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@tc.riken.jp  
PRIMERS  
Sequencing : T7  
LIBRARY  
Vector : pBACE3.6  
R.site 1 : BcORI  
R.site 2 : BcORI  
FEATURES  
source  
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Oy 484 CGCCGCTCCGAGCGAGCGAGAGGCGGCACTTTCAGATCCGAGGCGCTTC 543  
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 Db 646 CCC 587  
 Oy 604 CCGCGCGCGCGGCGCTACCTATGAGGCTGACACATCCGCACTCGGCAATGGGCT 663  
 Db 586 CCCCCCNCC 527  
 Oy 664 CGAGGACAGCGCTCGCGCTCGGCTCTCGGCACTCGGCTGAGAGGCGGCT 723  
 Db 526 CCC 467  
 Oy 724 CCGTCAAGAGCGCTCATCGACGAGGCTACATGAGAGAGATCTGTGTCAACGACTG 783  
 Db 466 CCC 407  
 Oy 784 GCTCTTGCGCTTCTCTCTCTAGTACCAACATCATGAGAGTGAACGCGTGAACCC 843  
 Db 406 CCC 347  
 Oy 844 GAGAGGATGAGGCTTCATCCGCGCTCGGCTGATCCGCTTCGCGAGAGAGGCGTGC 903  
 Db 346 CCGCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 287  
 Oy 904 GCAAGAGACCTTCGCGGATCAAGTGAACGAGCGGCGGCTTCCTCTCCGACCT 963  
 Db 286 CCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 227  
 Oy 964 CCGCGCTCTCTGAGTAAAC 982  
 Db 226 CCC 208

RESULT 3  
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 LOCUS P048-3-H10.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic,  
 genomic survey sequence.  
 ACCESSION CG753585  
 VERSION CG753585.1 GI:37978216  
 KEYWORDS GSS.  
 SOURCE Pristionchus pacificus  
 ORGANISM Pristionchus pacificus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
 Neodiplogasteridae; Pristionchus.  
 1 (bases 1 to 1277)  
 REFERENCE Strinivasan,J., Sinz,W., Jeesse,T., Wiggers-Perebolte,L., Jansen,K.,  
 Bunjef,J., van der Meulen,M. and Sommer,R.J.  
 An integrated physical and genetic map of the nematode Pristionchus  
 pacificus  
 TITLE Mol. Genet. Genomics 269 (5), 715-722 (2003)  
 JOURNAL 12884007  
 MEDLINE Contact: Sommer RJ  
 PUBMED Evolutionary Biology  
 COMMENT Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 Classes: BAC ends.  
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 /db\_xref="taxon:54126"  
 /clone\_lib="Ppa EcoRI BAC library"

/note="The library was generated by a partial digest of  
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 vector."

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 Oy 64 CGCGGCTTCTCGCGGCTGAGCGGAGTTCCTGAGCTCCGCAAGGCGCTTCGCGAGAA 123  
 Db 1208 CCGCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 1149  
 Oy 124 GCGCGTGGGAGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 183  
 Db 1148 CCC 1089  
 Oy 184 CACCTTGAACATGGGCGGCGGAGTGTCTCTCGCGGAGGATGTCGGGCGCGAGGT 243  
 Db 1088 NCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 1029  
 Oy 244 GCACATCGTGGCGGCGGCGGCGGCTTCGAGCGGCGGCTTCATGCGGCTTCGCTC 303  
 Db 1028 CCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 969  
 Oy 304 CGTGAAGAGCTCACCGAGTTCTTCTCGCGAGATGAGTACGAGTACGAGACACGG 363  
 Db 968 CCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 909  
 Oy 364 CATCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 423  
 Db 908 CCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 849  
 Oy 424 CGTGTCAAGGCGGCGGCGGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGG 483  
 Db 848 CCC 789  
 Oy 484 CGCGCGCTTCGAGCGGCGGCGGAGAGAGCGGCGGCGGCTTCGAGGCGGCGGCTTC 543  
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 Db 668 CCC 609  
 Oy 664 CGAGGACAGCGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 723  
 Db 608 CCCCCC--CCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 551  
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 Db 550 CCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 491  
 Oy 784 GCTCTTGCGCTTCTCTCTCTAGTACCAACATCATGAGAGTGAACGCGGCTGAAACCC 843  
 Db 490 CCC 431  
 Oy 844 GAGAGGATGAGGCTTCATCCGCTCGGCTGATCCGCTTCGCGAGAGAGGCGGCTGC 903  
 Db 430 CCC 371  
 Oy 904 GAGAGAGACCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 963  
 Db 370 NCC 311

QY 964 CCGGCGCTTC 973  
 Db 310 CCCCCCCCCC 301  
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 LOCUS P047-2-A01.za Ppa Ecoli BAC library Pristionchus pacificus genomic,  
 genomic survey sequence.  
 ACCESSION CG752479  
 VERSION CG752479.1 GI:37975985  
 KEYWORDS GSS.  
 SOURCE Pristionchus pacificus  
 ORGANISM Pristionchus pacificus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
 Neodiplogasteridae; Pristionchus.  
 REFERENCE 1 (bases 1 to 1601)  
 AUTHORS Srinivasan,J., Sinz,W., Jeease,T., Wiggers-Perebolte,L., Jansen,K.,  
 Buntjer,J., van der Meulen,M. and Sommer,R.J.  
 An integrated physical and genetic map of the nematode Pristionchus  
 pacificus  
 JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)  
 MEDLINE 22835951  
 PUBMED 12884007  
 COMMENT Contact: Sommer RJ  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 Class: BAC ends.  
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 /note="The library was generated by a partial digest of  
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 vector."  
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 Best Local Similarity 41.5%; Pred. No. 1.5e-12;  
 Matches 402; Conservative 0; Mismatches 567; Indels 0; Gaps 0;  
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 Db 1250 CCCCCCCCCCCCCCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 1191  
 QY 64 CGCGGGCTTCTCGCGCGCTGGCGGAGTTCTTGGCTCCCGCAAGGCGCTCGCGAAG 123  
 Db 1190 NCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 1131  
 QY 124 GCGCGTGGCGGAGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 183  
 Db 1130 CC 1071  
 QY 184 CACCTTGACATCGGCGCGGAGGTGCTCTCTCGCGAGGTGTCGCGCGCGCGCGAGT 243  
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 QY 244 GCAATCTGGCGCGGACCGGCTTGTGTGACCCCGCGCTCTCAATGCGCTTCGCTC 303  
 Db 1010 CC 951  
 QY 304 CGTGAAGAGCTCAACCGATCTTCTCTCGCGAGATTCAGTACGCGATCGAGACACCG 363  
 Db 950 CC 891

QY 364 CATCGCGCGCGCATCATCAAGTGGCCACACCGGAGCGACCCCGTTCCAGAGACT 423  
 Db 890 CCCCCCCCCCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 831  
 QY 424 GTGCTCAAGGCGCGCGCGCGCGCTTCCCTGCGACCGGCGTGGCGGTGACCAACAC 483  
 Db 830 CCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 771  
 QY 484 CGCGGCTTCGCGGCGGACGCGGAGAGAGAGGCGGCGGATCTTTCAGTTCGAGGCGCTTC 543  
 Db 770 CCGNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 711  
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 Db 470 CCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 411  
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 QY 904 CGAGAGACCTTCGCGGCGGATCACGTTGACCAACCGGCGGCTTCTTCCGACCTT 963  
 Db 350 CCGCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 291  
 QY 964 CCGGCGCTC 972  
 Db 290 CCCCCCCCCC 282  
 RESULT 5  
 AG340866 1565 bp DNA linear GSS 02-JUN-2004  
 LOCUS Mus musculus moJossinus DNA, clone:MSMg01-134A20.TJ, genomic survey  
 sequence.  
 ACCESSION AG340866  
 VERSION AG340866.1 GI:47914176  
 KEYWORDS GSS.  
 SOURCE Mus musculus moJossinus  
 ORGANISM Mus musculus moJossinus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1  
 AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.  
 BAC end Sequences of Library MSMg01  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1565)  
 AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan  
 (E-mail:hattori@gs.c.riken.jp, URL:http://hgp.gsc.riken.go.jp/,  
 Tel:81-45-503-9111, Fax:81-45-503-9170)  
 Clones are derived from the mouse BAC library MSMg01. For BAC  
 library availability, please contact Kuniya Abe (abe@rc.riken.jp).  
 Teukuda Institute, Bio Resource Center,  
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@rtc.riken.jp

## PRIMERS

Sequencing : TU

LIBRARY

Vector : pBACE3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

## FEATURES

source

location/Qualifiers

1..1565

/organism="Mus musculus molossinus"

/mol\_type="genomic DNA"

/sub\_species="molossinus"

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/clone="MSMG01-134A20.TU"

/sex="male"

/tissue\_type="mixture of kidney and spleen"

/clone\_lib="MSMG01 Mouse Male BAC Library"

## ORIGIN

Query Match 12.8%; Score 126; DB 9; Length 1565;

Best Local Similarity 42.4%; Pred. No. 1.9e-12;

Matches 411; Conservative 0; Mismatches 559; Indels 0; Gaps 0;

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DB  516  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 575
QY  124  GGGCGGTGGCGGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 183
DB  576  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 635
QY  184  CACCTTCAACATCGAGCGCGAGTGTCTCTCGCGAGTGTCCGCGCGCGCGAGAT 243
DB  636  NCCGNCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 695
QY  244  GCACATCGTGGCGCGCAGCGGCTTGTGTGACCCGCGGCTTCTCATGGGCTCTGCT 303
DB  696  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 755
QY  304  CGTGAAGAGCTCACCCAGTTCTTCTCGCGAGATCCAGTACGAGATGAGAGACCGG 363
DB  756  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 815
QY  364  CATCGCGCGCGATCATCAAGTGGACACACCGGCAAGGCAACCCGTTCCAGAGCT 423
DB  816  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 875
QY  424  CGTGTCAAGGCGCGCGCGCGCTCTCTCGCACCGGCGTGGAGTACCAACCAAC 483
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DB  996  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1055
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QY  784  GCTTGGGCTTCTTCTTCTTACGTGACCAATATGAGACGTATGAGACCGGTGAACC 843
DB  1236  NCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1295
QY  844  GAGAGCATGAGCTTATCGGCTCGGCTGATCCGCTTCTCGCGAGAGGCGTGC 903
DB  1296  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1355
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DB  1356  CCGNCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 1415
QY  964  CCGGCGCTTC 973
DB  1416  CCGNCCCGCC 1425

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## RESULT 6

CG746709/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

Class: BAC ends.

Class: BAC ends.

Class: BAC ends.

Class: BAC ends.

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## ORIGIN

Query Match 12.8%; Score 126; DB 9; Length 1567;

Best Local Similarity 40.1%; Pred. No. 1.9e-12;

Matches 390; Conservative 0; Mismatches 583; Indels 0; Gaps 0;

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QY  1  CCGCCGATCAACATCTCCAGGCGGCTTCACTCAACCCAGAGCAATCTGGGCTC 60
DB  1487  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1428
QY  61  CTCGCGGCTTCTCTCGCGCTTGCGAGTCTTGGCTTCCGCAAGGCGCTTGGCGGA 120
DB  1427  NCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 1368

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OY	121	GAAGGCGCTGTGCGGCGCTTCGCGCGGCGCCGCGCGCGGTGGCGACCATGTGGAGCT	180
Db	1367	CC	1308
OY	181	GTGCACCTTTCGACATCGGCGCGGACGATGTCCTCTCGCGAGAGTGTCCCGGCGCGCA	240
Db	1397	CCCCCCNCCNCC	124
OY	241	CGTGACATCTGTGCGCGCCACCGGCGCTGTGTTGACCCCGCGCTCTCCATGCGGCTTCG	300
Db	1247	CC	1188
OY	301	CTCGGTGAGAGAGTCACCCAGTTCTCTCGCGAGATCCAGTACGAGATGAGAGAC	360
Db	1187	NCC	1122
OY	361	CGGACCTCGCGCGGACATCATCAAGTGGCCACACCGGCAAGGACACCCCGTTCCAGA	420
Db	1127	CC	1068
OY	421	GCTGTGTCTCAAGGCGCGCGCGCGCTCTCGCGCACCGGCGTGGCGGTACCAACCA	480
Db	1067	CC	1008
OY	481	CACCGCGCGCTCCAGCGGAGAGGAGAGAGGCGCGCATCTTCAGATTCGAGAGGCT	540
Db	1007	CCCNCC	948
OY	541	CTCCCCGTTCGCGCGTGTGATGGCCACTCGGACGACACCGACGACTCTCTTACTTCAC	600
Db	947	CC	888
OY	601	CGCCCTGCGCGCGGCGGCTACTATGAGGCTTCGACACATCCCGCACTCGGCATCGG	660
Db	887	CCCCCCNCCCCCCCCCCCGCAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	828
OY	661	CCTGAGAGCAACGCTTCGCGGTCCGCTCTCTGAGCATTCGCTCTTGAGACCCCGCGC	720
Db	827	CCCCNCC	768
OY	721	CCTCTGTCAAGGCGCTCATGACACGAGGCTACATGAAAGCATCTCTGTGTCCAAGA	780
Db	767	CC	708
OY	781	CTGGCTTTCGCGCTTCTCTCTACTGATGCAACATCATGACGTGATGACCGGATGA	840
Db	707	CCCCCCCCNCCNCCCCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC	648
OY	841	CCCGAGCGGACATGGCTTTCATTCGCGCTCGCGGTGATCCCGTTCTTCGCGAGAGAGCGT	900
Db	647	CC	588
OY	901	GCGGAGAGACCTTCGCGGCGCATACCGTGAACAAACCGGCGCGCTTCTCTCCCGAC	960
Db	587	CCCCCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC	528
OY	961	CCTCGGCGCTTC	973
Db	527	CCCCCCCCCCCC	515

RESULT	7
LOCUS	CC290874
DEFINITION	CH261-172N5_sp6.1 CH261 Gallus gallus genomic clone genomic survey sequence.
ACCESSION	CC290874
VERSION	CC290874.1 GI:30662315
KEYWORDS	GSS:
SOURCE	Gallus gallus (chicken)
ORGANISM	Gallus gallus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	Phasianinae; Gallus. 1 (bases 1 to 1695)	Kremetzki, C., Higgishoeham, J., Wylie, K., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.	Gallus gallus BAC End Reads	Unpublished (2003)
	Contact: Richard K. Wilson	Genome Sequencing Center	Washington University School of Medicine	Email: submissions@wustl.edu
	Insert Length: 182000	Std Error: 0.00	Seq primer: Sp6 ATTGAGTGAACACTTAAG	Class: BAC ends
	High quality sequence start: 26	High quality sequence stop: 136.	Location/Qualifiers	
	1..1695		/organism="Gallus gallus"	
	/mol_type="genomic DNA"		/strain="Red Jungle Fowl"	
	/db_xref="taxon:9031"		/clone="CH261-172N5"	
	/sex="female"		/cell_line="UCD001, inbred 256"	
	/clone_id="CH261"		/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI; CH261 Female Chicken library - For library and clone ordering information: <a href="http://www.chori.org/bacpac">http://www.chori.org/bacpac</a> "	
ORIGIN	Query Match	12.8%; Score 125.6; DB 8; Length 1695;		
	Best Local Similarity	45.0%; Pred. No. 2.2e-12;		
	Matches 436; Conservative	0; Mismatches 529; Indels 4; Gaps 1.		
QY	5	CCGATACCAATCTCGAAGCCGGCTTACCTCACCAGACACATGTGGGCTCTCC	64	
DB	326	CCCCCGGGCCCCCGCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	385	
QY	65	GCCGAGCTTCCTCCGGGCGCTGGCGCGAGTTCTTCGGCTCGCGAAGGCCCTCGCGAAG	124	
DB	386	CCCCCCCCCGCCCGCC	445	
QY	125	GCCTGTGCGGCTTCGCGCGCGCCGCGCGCGCGCGGTGCGCACCATGTAAGTGTCC	184	
DB	446	CC	505	
QY	185	ACCTTCGACATCGGCGCGAGCTGTCTCTCTCGCGGAGTGTCCCGCGCGCGAGCTG	244	
DB	506	CCCGCG	565	
QY	245	CACATCTGTGGCGCGCACCGGCTCTGTGTGAACCGCGCTCTCATAGGCTCCGCTCC	304	
DB	566	CC	625	
QY	305	GTGAGAGAGCTCACCGAGTTCTTCTCTCGCGAGATTCAGTACGAGATGAGAACCGGC	364	
DB	626	CCCCCCCCCGCCCGCCCCCCCCCCCCCCCCCCCCCCCCCGCGCGCGCGCGCGCG	685	
QY	365	ATCGCGCGCGCATTCATTCAGTGAAGTGAACACCGGACAGGCCACCCGCTTCAGAGCTC	424	
DB	686	CCCGCGCGCGCCCG	745	
QY	425	GTGCTCAAGGCGCGCGCGCGCGCGCTTCTTCGCGCACCGCGGTGCGGTAACACCCACAC	484	
DB	746	CGNCG	805	
QY	485	GCGCGCTCCAGCGAGCGAGCGAGCGAGCGCGCATCTTCAGATCGAGGCGCTCTCC	544	
DB	806	GGCGCCCGCCCG	865	
QY	545	CGGTCCCGCGGTGATCGAGCGCACTTCGACGACCGAGCGACGACGACCTCTCTACCTACCGCC	604	
DB	866	GGCG	925	

Oy 605 CTCGCCGCGCGGCTACTCATCGGCTCGACCATCCGCACTCCGCACTCGGCTC 664  
Db 926 CCCGCCGCGC-----CCCCCCCCCNCNCCCCCCCCCCCCCCCCCCCCCCCC 981  
Oy 665 GAGGACAACGCGCTCGGCTCGGCTCTCTCGGCACTCGGCTCGGAGACCGCGCTC 724  
Db 982 CCGCGCCCCCGGCGCGCCCCCCCCCCCCCCCCCCCCCCCCCNCNCCCCCCCCCG 1041  
Oy 725 CTCATCAAGGCGCTCATGACGAGGCTACATGAAGCAGATCTCTGTCCAGACTCG 784  
Db 1042 CCCCCCNCNCCCCCGCGCCCCCCCCCCCCCCCCCCCCCCCCCGCGCGCCCCCCC 1101  
Oy 785 CTCCTCGGCTTCTCTCTCACTGACCAACATCATGAGCTGATGAGCGGCTGAACCG 844  
Db 1102 CCGCGCCCCCCCCCCCCCNCNCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1161  
Oy 845 GACGCGCATGCGCTTCATCGCGCTCGGCTGATCCGCTTCTCGGAGAGGCGCTGCG 904  
Db 1162 CCCCCCNCNCCCCCG 1221  
Oy 905 CAGGAGACCTTCGCGGCGATCAGCGTGAACCAACCGCGCGCTTCTCTCCGACCTC 964  
Db 1222 CGCGCGCCNCCCGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1281  
Oy 965 CGCGCGCTCG 973  
Db 1282 CGCGCGCGCG 1290

RESULT 8  
AG448338/c 1874 bp DNA linear GSS 03-JUN-2004  
LOCUS Mus musculus molossinus DNA, clone:MSMg01-332B03.TU, genomic survey  
DEFINITION  
ACCESSION AG448338 GI:48091401  
VERSION AG448338.1  
KEYWORDS GSS.  
SOURCE Mus musculus molossinus  
ORGANISM Mus musculus molossinus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
TITLE BAC and Sequences of Library MSMg01  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1874)  
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
TITLE Direct Submision  
JOURNAL Submitted (17-NOV-2003) Maehira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan  
1-7-22 Suhiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel:81-45-503-9111, Fax:81-45-503-9170  
E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/  
Clones are derived from the mouse BAC library MSMg01. For BAC  
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
Tsukuba Institute, Bio Resource Center,  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyadai, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@rtc.riken.jp

## COMMENT

PRIMERS  
Sequencing : TU  
LIBRARY Vector : pBACE3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI.

FEATURES  
source

1. 1874  
Location/Qualifiers  
/organism="Mus musculus molossinus"  
/mol\_type="genomic DNA"  
/sub\_species="molossinus"  
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ORIGIN  
Query Match 12.8%; Score 125.4; DB 9; Length 1874;  
Best Local Similarity 41.3%; Pred. No. 2,48-12;  
Matches 402; Conservative 0; Mismatches 571; Indels 0; Gaps 0;  
/clone="MSMg01-332B03.TU"  
/sex="male"  
/tissue type="mixture of kidney and spleen"  
/clone\_lib="MSMg01 Mouse Male BAC Library"

Oy 1 CGGCGCATACCATCTTCGAGCGCGGCTTCACTTCAACCCAGAGACATCTGGGCTC 60  
Db 1822 CCG 1763  
Oy 61 CTCGCGCGGCTTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120  
Db 1762 CCG 1703  
Oy 121 GAAAGCGGCG 180  
Db 1702 CCG 1643  
Oy 181 GTCCACTTTCGACATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
Db 1642 CCG 1583  
Oy 241 GGTGCAATCGTGGCG 300  
Db 1582 CCG 1523  
Oy 301 CTCGCGGAGAGGCTCAACGATTTCTTCTCGGAGATCCAGTACGAGCATCGAGACAC 360  
Db 1522 CCG 1463  
Oy 361 CGGCACTCGCGCGCGCGCATCATCAAGTGGCCACCAACGCGGAGGCGCGCTTCAGAGA 420  
Db 1462 CCG 1403  
Oy 421 GCTGTGTCAAGGCG 480  
Db 1402 CCG 1343  
Oy 481 CACGCGCGCTTCCAGCGCGAGCGAGCAGCAGGCGCAGCTTCGATCGAGGCGCT 540  
Db 1342 CCG 1283  
Oy 541 CTCGCGGTCGCGCGGTGCGCATCGGCACTCGAGCAGCAGCAGCAGCAGCAGCAGC 600  
Db 1282 CCG 1223  
Oy 601 CGCGCTGCGCGCGCGCGCGCTACCTCATGCGCTGAGCAGCATCCGCGCATCGG 660  
Db 1222 CCG 1163  
Oy 661 CCGGAGGACAACGCGCTCGGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720  
Db 1162 CCG 1103  
Oy 721 CTCCTCATCAAGGCGCTCATGACGAGGCTACATGAAGCAGATCTCTGTCCAGAGA 780  
Db 1102 CCG 1043  
Oy 781 CTGCGCTCTTGGGCTTCTCTCTACGTGACCAACATCATGAGCGATGAGACCGGCTGA 840  
Db 1042 CCG 983  
Oy 841 CCGGAGGCGCATGCGCTTTCATTCGCGCTCGGCTGATCCGCTTCTTCGCGAGAGGCGT 900  
Db 982 CCG 923  
Oy 901 CGCGGAGAGACCTTCGCGCGGATCAACGTGACCAACGCGGCGCGCTTCTCTCGGAC 960  
Db 922 CCG 863

Qy 961 CCTCGGCGCTCC 973  
Db 862 CCCCCCCCCCCC 850

RESULT 9  
AG363808 2041 bp DNA linear GSS 03-JUN-2004  
LOCUS Mus musculus molossinus DNA, clone:MSMg01-165M06.TU, genomic survey  
DEFINITION  
ACCESSION AG363808  
VERSION AG363808.1 GI:47975013  
KEYWORDS GSS.  
SOURCE Mus musculus molossinus  
ORGANISM Mus musculus molossinus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.  
TITLE BAC end Sequences of Library MSMg01  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2041)  
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.  
TITLE Direct Submission  
JOURNAL  
REFERENCE Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Saitoh-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the mouse BAC library MSMg01. For BAC  
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
Tsukuba Institute, Bio Resource Center,  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyadai, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@rtc.riken.jp  
PRIMERS  
Sequencing : TJ  
LIBRARY : PBACE3.6  
Vector : EcoRI  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI.  
FEATURES  
source Location/Qualifiers  
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/organism="Mus musculus molossinus"  
/mol\_type="genomic DNA"  
/sub\_species="molossinus"  
/db\_xref="taxon:57486"  
/clone="MSMg01-165M06.TU"  
/sex="male"  
/tissue\_type="mixture of kidney and spleen"  
/clone\_lib="MSMg01 Mouse Male BAC Library"

ORIGIN  
Query Match 12.7%; Score 125; DB 9; Length 2041;  
Best Local Similarity 46.9%; Pred.No.2.8e-12;  
Matches 460; Conservative 0; Mismatches 515; Indels 6; Gaps 2;  
Qy 1 CGGCCCATCACTTCGAGGCGCGCTTCACTTCAACCAAGGACATCTGGGCTC 60  
Db 881 CGGCCCGCGCGCCCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 940  
Qy 61 CTCGCGCGGCTTCTCCGCGCTTCGCGCGCGAGTTCTTCCGCGCGCGCGCGCGCGA 120  
Db 941 CCG 1000  
Qy 121 GAAGCGCGCTTCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 180  
Db 1001 GCG 1060  
Qy 181 GTCACCTTGAACATCG 235

Db 1061 CCCCCCG 1120  
Qy 236 GCGACATGACATATGAGCG 295  
Db 1121 GCG 1180  
Qy 296 CTCGCTTCGTGAGAGAGCTCACCAAGTTCTTCTTCGCGAGATTCAGTACGCGATGAG 355  
Db 1181 CG 1240  
Qy 356 GACACCGGATTCG 415  
Db 1241 GCG 1300  
Qy 416 CAGAGCTCTGTG-CTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 474  
Db 1301 GCG 1360  
Qy 475 CACCGACACCG 534  
Db 1361 CCG 1420  
Qy 535 GGGCGCTTCG 594  
Db 1421 CCG 1480  
Qy 595 CCGTACCG 654  
Db 1481 CG 1540  
Qy 655 CATGCGCTTGAAGACACGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 714  
Db 1541 CG 1600  
Qy 715 CG 774  
Db 1601 CG 1660  
Qy 775 CACGACTGCTCTTTCGCGCTTCTCTCTCACTGACCAACATGACGATGATGACCG 834  
Db 1661 CGCGCTCG 1720  
Qy 835 GGTGAACCGGAGCGCATGCGCTTTCATTCGCGCGCGCGCGCGCGCGCGCGCGCG 894  
Db 1721 CG 1780  
Qy 895 GGGCGTGCAGAGAGACCGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 954  
Db 1781 GCG 1840  
Qy 955 CCGGACCTTCG 975  
Db 1841 GCG 1861

RESULT 10  
CK162505 1107 bp mRNA linear EST 05-DEC-2003  
LOCUS FGAS015100 Triticum aestivum FGAS: Library 4 Gate 8 Triticum  
DEFINITION  
ACCESSION CK162505  
VERSION CK162505.1 GI:38991779  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poidaeae; Triticaceae; Triticum.  
REFERENCE  
AUTHORS Allard,F., Crosby,W.L., Danyluk,J., Budes,F., Frick,M., Gaudet,D.,  
Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,  
Linka,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilsson,D.,  
Penniket,C., Roach,J.L. and Sarnan,F.



TITLE  
Functional Genomics of Abiotic Stress in Wheat and Canola Crops  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Wm L Crosby  
Bioinformatics  
University of Saskatchewan, Department of Computer Science  
1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
Saskatchewan, S7N 5A9, Canada  
Tel: 306 966 1769  
Fax: 306 966 2033  
Email: fgas.ests@usask.ca

This sequence is the direct result of the base calling software  
Phred (default parameters). It is the raw base calls. To aid in the  
identification of the high quality insert the software Lucy  
(default parameters) has been run on this sequence. Lucy identified  
the region [3,186].  
Plate: L4B005 row: C column: 12.

FEATURES  
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/mol\_type="rRNA"  
/db\_xref="taxon:4565"  
/clone\_lib="Triticum aestivum FGAS: library 4 Gate 8"  
/note="Organ: Crown and leaf; Vector: PCMV.SPORT6;  
Conditions for growth: Seeds were germinated in a  
water-saturated mix (50% black earth and 50% Promix) in a  
growth chamber for 7 days under an irradiance of 200 mmol  
m-2 sec-1. The temperature was maintained at 20 degrees C  
with a 15-hr photoperiod under a relative humidity of 70%.  
After this period watering of plants was stopped. Four  
time points were sampled during a two week period; the  
first after wilting was observed and the last, two weeks  
later, consisted of live crown and leaf tissue (leaf  
tissue that was yellow was not included in sampled  
material). First strand synthesis in this library was done  
in the presence of methylated dCTP thereby protecting from  
internal cleavage with NotI."

ORIGIN

Query Match 12.7% Score 124.4; DB 7; Length 1107;  
Best Local Similarity 39.7%; Pred. No. 3,6e-12;  
Matches 384; Conservative 0; Mismatches 581; Indels 3; Gaps 1;

6 CGATCACCATCTCCGAGCGCGCTTACACCCACGAGACATCTGCGCTCTCCG 65  
123 GCGGACAGCTTCTCGGCGCTTCTCGGAGCTCATCTGTCCTCCCGCGACGCGCC 182  
66 CCGGCTTCTCTCGGCGCTGCGGAGTTCTTCTGCTCCGCAAGGCTTCCGGAAG 125  
183 CCGGCG 242  
126 CCGGCG 185  
243 GCGGAGGCG 302  
186 CTTTGACATCTCGGCGCGCGCGCTTCTGCGCGAGTGTCTCCGCGCGCGCGAGTGC 245  
303 NNNNNCCCCCG 362  
246 ACATGTGCGCGCGCGCGCGCGCTTCTGCTGCGCGCGCTTCTGCGCGCTCTCG 305  
363 CCGGCG 422  
306 TGGAGAGGTCAACCGAGTTCTTCTCGGAGATTCAGTACGCGATTCAGAGACACCGGA 365  
423 CCGGCG 482  
366 TCCG 425  
483 CCGGCG 542  
426 TGTCTAAGGCGCGCGCGCGCGCTTCTTCTGCGCAACGCGGTGCGTGAACCAACCG 485  
543 CCGGCG 602

486 CCGGCTCCAGCGGAGCGGCGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 545  
603 CCGGCG 662  
546 CCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 605  
663 NNNCG 719  
606 TCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 665  
720 NNNCG 779  
666 AGGACAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 725  
780 NNNCG 839  
726 TCAATCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 785  
840 CCGGCG 899  
786 TCTTGGCTTCT 845  
900 CCGGCG 959  
846 ACGGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 905  
960 CCGGCG 1019  
906 AGGACAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 965  
1020 CCGGCG 1079  
966 GCGGCTTC 973  
1080 CCGGCGCGCG 1087

RESULT 11  
AG349830/c 1193 bp DNA linear GSS 02-JUN-2004  
LOCUS  
DEFINITION  
MUS musculus molossinus DNA, clone:MSM901-146D19.T7, genomic survey  
sequence.  
ACCESSION  
AG349830  
VERSION  
AG349830.1 GI:47923140  
KEYWORDS  
GSS.  
SOURCE  
MUS musculus molossinus  
MUS musculus molossinus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
BAC end Sequences of Library MSM901  
Unpublished  
JOURNAL  
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
Direct Submission  
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Tsukuba-shi, Tsukuba, Ibaraki, Japan  
E-mail: hattori@ipc.riken.jp, URL: http://hgp.gsc.riken.go.jp/  
Tel: 81-45-503-9111, Fax: 81-45-503-9170  
Clones are derived from the mouse BAC library MSM901. For BAC  
library availability, please contact Kunita Abe (abe@ipc.riken.jp).  
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyadai, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@ipc.riken.jp

PRIMERS  
Sequencing : T7  
LIBRARY  
Vector : PBACE3.6

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R.Site 1 : ECORI
R.Site 2 : ECORI.
FEATURES Location/Qualifiers
source    1. .1193

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ORIGIN

QY 84 GAGCGGCGATGGCGCTTCATCCGGCTCGGGGTATCCCGTCTCGGCGAAGAGGGCGTGGC 903  
 Db 315 NCNNNNCCNCCCCCNNNCCCCCCCCCNCCNCCNCCCCCNCCCCCCCCCCCCCCCCCCCCCN 256  
 QY 904 GCAGAGACCTCTGCGCGGCGATCAGCGGTAGCAACCGGGCGGCTTCTCTTCCCGAACCT 963  
 Db 255 NCCCNCCCCCNCCNCCNCCCCCCCCCCCCCCCCCCCCCNCCCCCCCCCCCCCCCCCCCCCNCC 196  
 QY 964 CCGGCGCTCC 973  
 Db 195 CCGCNCCNCC 186

RESULT 12	
CG748176	
LOCUS	CG748176 1471 bp DNA linear GSS 24-OCT-2007
DEFINITION	P0421-A01.2a Ppa Score BAC library <i>Pristionchus pacificus</i> genomic.
ACCESSION	CG748176
VERSION	CG748176.1 GI:37969102
KEYWORDS	GSS.
SOURCE	<i>Pristionchus pacificus</i>
ORGANISM	<i>Pristionchus pacificus</i>

**COMMENT**

Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Semmelweisstr. 37-39, Tübingen D-72076, Germany  
Tel.: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
Class: BAC ends.

**ORIGIN**

	Query Match	12.6%	Score 124;	DB 9;	Length 1471;
	Best Local Similarity	42.0%	Pred. No. 4,2e-12;		
	Matches 409;	Conservative 0;	Mismatches 554;	Indels 0;	Gaps 0
QY	1 CGAGCCGATACCACTTCGCCGAGCGCGCTTACCTTCACCACGAGCACAATTGGAGCTTC	60			
Db	186 CMCCCCCCCCNCNCCCCCNMNNCCCCCCCCNCCCCCCCCCCCCCCCCCCCCCCCCCCCC	245			
QY	61 CTCGCGCGAGCTTCCTCGCGGCGCTGAGCGAATTCTTGAGGTCCCGGAAGCCCTTCGCCCA	120			
Db	246 CCCCCNCNCCNCC	305			
QY	121 GAAGGCGGTGCAGGCGCTTCGCGCGGCGCGCGCGCGCGCGCGAGTCGAGCACATCTGAGACT	180			
Db	306 CC	365			
QY	181 GTTCACCTTTGCAGCATCGGCGCGGACGATGTCTCTTCGCGGAGAGTGTCCCGCGCGGCCA	240			
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VERSION			CG753270	
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REFERENCE			1 (bases 1 to 1616)	
AUTHORS			Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,	
TITLE			Buntjer,J., van der Meulen,M. and Sommer,R.J.	
JOURNAL			An integrated physical and genetic map of the nematode Pristionchus	
MEDLINE			Pacificus	
			MoJ. Genet. Genomics 269 (5), 715-722 (2003)	
			22815951	

PUBLISHED 12884007  
 COMMENT Contact: Sommer RJ  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@uebingen.mpg.de  
 Class: BAC ends.  
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 950 CC 89  
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ACCESSION	CG748837
VERSION	CG748837.1 GI:37969763
KEYWORDS	GSS.
SOURCE	Pristionchus pacificus
ORGANISM	Pristionchus pacificus

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
1 (bases 1 to 1970)	Srinivasan,J., Sinz,W., Jeease,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., Van der Meulen,M. and Sommer,R.J.	An integrated physical and genetic map of the nematode <i>Pristionchus pacificus</i>	Mol. Genet. Genomics 269 (5), 715-722 (2003)	22835951	12884007	Contact: Sommer RJ

**FEATURES**  
**source** 1..1970  
**location/Qualifiers**  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel.: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 Class: BAC ends.  
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[illegible]

RESULT 15	
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ACCESSION	Jc091860
VERSION	CB908860
KEYWORDS	CB908860.1 GI:30123518
SOURCE	EST.
ORGANISM	Hypocrea jecorina (anamorph: Trichoderma reesei)
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
	Hypocreales; Hypocreatales; Hypocreales; Hypocreales; Hypocrea.
REFERENCE	1 (bases 1 to 1087)
AUTHORS	Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
	Dunn-Coleman, N.S., Goedegebuurt, F., Houtek, T.D., England, G.J.,
	Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 5378673 seqs, 295022984 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	982	100.0	1082	US-09-881-165-4	Sequence 4, Appli
3	628	64.0	3713	US-10-272-351-29	Sequence 29, Appli
4	624.6	63.6	1029	US-09-791-138A-3	Sequence 3, Appli
5	566.8	57.7	1071	US-10-477-469-6	Sequence 6, Appli
6	566.8	57.7	1155	US-10-477-469-5	Sequence 5, Appli
7	565.2	57.6	1155	US-10-477-469-8	Sequence 8, Appli
8	562	57.2	1155	US-10-477-469-7	Sequence 7, Appli
9	167.4	17.0	978	US-10-282-122A-25658	Sequence 25658, A
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11	148.8	15.2	918	US-10-282-122A-26226	Sequence 26226, A

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C	13	136.2	13.9	985	18	US-10-363-345A-31408	Sequence 31408, A
C	14	122.6	12.5	1296	17	US-10-398-221-610	Sequence 610, App
C	15	122.6	12.5	1311	17	US-10-398-221-613	Sequence 613, App
C	16	122.6	12.5	319630	17	US-10-398-221-7	Sequence 7, Appli
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C	19	119.2	12.1	125401	18	US-10-203-295-35	Sequence 35, Appli
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C	24	114.8	11.7	88400	18	US-10-844-716-1	Sequence 1, Appli
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C	35	109.6	11.2	7536	10	US-09-940-316B-1	Sequence 1, Appli
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## ALIGNMENTS

RESULT 1  
US-10-727-010-1  
; Sequence 1, Application US/10727010  
; Publication No. US20040250298A1  
; GENERAL INFORMATION:  
; APPLICANT: Pinkerton, T. Scott  
; APPLICANT: Howard, John A.  
; APPLICANT: Wild, Jim R.  
; TITLE OF INVENTION: Methods for Selecting and Screening for Transforms  
; FILE REFERENCE: P05574US01  
; CURRENT APPLICATION NUMBER: US/10/727,010  
; CURRENT FILING DATE: 2003-12-03  
; PRIOR APPLICATION NUMBER: US 60/430,626  
; PRIOR FILING DATE: 2002-12-03  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 982  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence originally obtained from Flavobacterium sp., Genbank  
; OTHER INFORMATION: accession number M29593. Sequence translated and back-translated  
; OTHER INFORMATION: with BACKTRANSLATE (Misc. GCG, ver. 9). Deleterious sequences  
; OTHER INFORMATION: removed with FINDPATTERN (Misc. GCG, ver. 9).

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Dd	961	CTCCGCGGCTCTGTAGTTAAC	982

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1  APPLICANT: BAILEY, MICHELE
2  APPLICANT: CASTEL, FRANS VAN
3  APPLICANT: WANG, HUANG
4  APPLICANT: WANG, MICHAEL
5  APPLICANT: WOODARD, SUSAN
6  TITLE OF INVENTION: METHOD OF INCREASING RECOVERY OF HETEROLOGOUS ACTIVE
7  TITLE OF INVENTION: ENZYMES PRODUCED IN PLANTS
8  FILE REFERENCE: 10032R
9  CURRENT APPLICATION NUMBER: US/09/881,165
10 CURRENT FILING DATE: 2001-06-14
11 PRIOR APPLICATION NUMBER: 60/211,732
12 PRIOR FILING DATE: 2000-06-15
13 NUMBER OF SEQ ID NOS: 5
14 SOFTWARE: PatentIn Ver. 2.1
15 SEQ ID NO 4
16     LENGTH: 1082
17     TYPE: DNA
18     ORGANISM: Artificial Sequence
19     FEATURE:
20 OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA encoding
21 OTHER INFORMATION: Organophosphate Hydrolase
22 US-09-881-165-4

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US-09-881-165-4  
; Sequence 4, Application US/09881165-4  
; Publication No. US20020039772A1  
; GENERAL INFORMATION:  
; APPLICANT: HOOD, ELIZABETH  
; APPLICANT: HOWARD, JOHN



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## RESULT 3

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; Sequence 29, Application US/10272351  
; Publication No. US20040005673A1  
; GENERAL INFORMATION:  
; APPLICANT: Jarell, Kevin  
; APPLICANT: Turczyk, Brian  
; TITLE OF INVENTION: System for Manipulating Nucleic Acids  
; FILE REFERENCE: 2003320-0013  
; CURRENT APPLICATION NUMBER: US/10/272,351  
; NUMBER OF SEQ ID NOS: 43  
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; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Presents the  
; OTHER INFORMATION: nucleotide sequence.  
US-10-272-351-29

Query Match 64.0%; Score 628; DB 17; Length 3713;  
Best Local Similarity 77.9%; Pred. No. 1.5e-131;  
Matches 757; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

Qy 1 CGGCGCATCACCATCTCCGAGCGCGCTTCAACCCCTCACCCAGAGACATCTGCGGCTC 60  
Db 139 CGGCTCTATCAATCTCTGAGCGGCTTTCACACTGATCTACAGACATCTGCGGCGAG 198  
Qy 61 CTCGCGCGGCTTCTCTCCGCGCTTCGCGGAGTCTTTCGCTCCCGGAGGCGCTTCGCGCA 120  
Db 199 CTCGCGAGGATCTTTCGCGCTTTCGCGGAGTCTTTCGAGGCGGAGGCTTTCGCGCA 258  
Qy 121 GAAAGCGGCGGCGCTTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
Db 259 AAGAGCTGAGAGAGATTCG 318  
Qy 181 GTCCACCTTCGACATGCGCGCGCGAGCGTGCCTCCCTCGCGGAGGATTCGCGGCGCGCG 240  
Db 319 GTTCGATTTTCGATATGCTGCGGAGCTGATTTATTTGCGCGAGGTTTCGCGGCTGCCA 378  
Qy 241 CGTGACATCTGCGCGCGCGAGCGGCTTCGCTTCGAGCCGCGCTCTCATGCGGCTTCG 300  
Db 379 CGTTATATCTGCGCGCGCGAGCGGCTTCGCTTCGAGCCGCGCATTTTCGATGAGTGA 438  
Qy 301 CTCGCGGAGAGCTTACCAAGTCTTCTCTCGCGGAGATTCGATAGGAGTGAAGAGAC 360  
Db 439 GAGTGAAGAGAGCTTACCAAGTCTTCTCTCGCGGAGATTCGATAGGAGTGAAGAGAC 498

Qy 361 CGGATCCGCGCGGATCATCAAGTGAACCAACCGGAGGACCCCGCTTCAGAGA 420  
Db 499 CGGATTTAGGCGGCGCATTTATAGTGGCGAGCAACAGGAGAGAGAGAGAGAGAGAG 558  
Qy 421 GCTGTGCTCAAGGCGCGCGCGCGCTTCTCTCGCGACCGGCGTGGAGTGAACCA 480  
Db 559 GTTATGTTTAAAGGCG 618  
Qy 481 CACGCGCGCTCCCGAGCGGAGCGAGAGAGGCGCGCATCTTCGATCCGAGGCGCT 540  
Db 619 CAGGAGAGAGTCAAGCGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 678  
Qy 541 CTCCCGCTCCGCGGCTGATCGAGCGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 600  
Db 679 GAGCGCGCTCAAGGAGTTCGATGATGATGATGATGATGATGATGATGATGATGAT 738  
Qy 601 GCGCTTCGCGCGCGCGGCTTCATGAGCGCTGAGCAACATCCGCGACCTCCGCAATCG 660  
Db 739 GCGCTTCGCGCGCGGAGTACCTCATGATGATGATGATGATGATGATGATGATGAT 798  
Qy 661 CCTGAGAGCAACGCGCTCGCGGTCGCGCTCCGCGCATCCGCTCTGAGAGAGAGAG 720  
Db 799 TCTAAGAGATTAAGGCTGAGAGATTCGCTCTGAGAGATTCGCTCTGAGAGAGAGAG 858  
Qy 721 CCTCTCATCAAGGCGCTCATGACCAAGGCTACATGAAGAGATCTCTGTCCAAACA 780  
Db 859 TCTCTTATCAAGGCGCTCATGACCAAGGCTACATGAAGAGATCTCTGTTCGAAAGA 918  
Qy 781 CTGGCTCTTCGCGCTTCTCTCTCTACGTGACCAACATCATGAGAGTGAACCGGCTGA 840  
Db 919 CTGGCTCTTCGCGCTTCTCTCTCTACGTGACCAACATCATGAGAGTGAACCGGCTGA 978  
Qy 841 CCCGAGCGGATGAGCTTCATCCGCGCTCGGCTGATTCGCTTCGCGGAGAGAGAG 900  
Db 979 CCCGAGCGGATGAGCTTCATCCGCGCTCGGCTGATTCGCTTCGCGGAGAGAGAG 1038  
Qy 901 GCGGAGAGAGACCTTCGCGGAGATCAAGGCTGAGCAACCGGCGCGCTTCTCTCCGAG 960  
Db 1039 CCCAG 1098  
Qy 961 CCTCGCGCTCT 972  
Db 1099 CTTCGCGCGCTC 1110

## RESULT 4

US-09-791-138A-3/C  
; Sequence 3, Application US/09791138A  
; Publication No. US20040106178A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jun  
; APPLICANT: Ackerman, Eric  
; TITLE OF INVENTION: Proteins in a Porous Support  
; FILE REFERENCE: E-1741  
; CURRENT APPLICATION NUMBER: US/09/791,138A  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 3  
; LENGTH: 1029  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: The organism is unknown per ATCC (#67778)  
US-09-791-138A-3

Query Match 63.6%; Score 624.6; DB 11; Length 1029;  
Best Local Similarity 77.5%; Pred. No. 1e-130;  
Matches 756; Conservative 0; Mismatches 219; Indels 0; Gaps 0;

Qy 2 GCGCGGATCACCATCTTCGAGGCGCGGCTTACCTTCACCCAGAGACATCTTCGCGCTCC 61  
Db 977 GGTCTATCAATCTTCGAGGCGCGGCTTTCACCTGATCAAGAGACATCTTCGCGGAC 918

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Qy 62 TCCGCGGCTTCTCTCCGCGCTGAGCGAGTTCCTCGGCTCCCGAGAGCCCTCCGCGAG 121
Db 917 TCGGCAAGATTCCTCGTGTCTGGCCAGAGTTCTTCGGTAGCGGAAAGCTCTACGCGGA 858
Qy 122 AAGCGCGTGGCGGCTCCGCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 181
Db 857 AAGCGTGTAGAGAGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 798
Qy 182 TCCACCTTCGACATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 241
Db 797 TCGACTTCGATATCGGTGCGGACGTCAGTTATTTGGCCGAGGTTTCGCGGCTCCGAC 738
Qy 242 GTGCAATGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 301
Db 737 GTTCATATCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 678
Qy 302 TCCGTGAGAGAGCTACCCAGTTCTTCTCCGCGAGATTCAGTAGGCAATCGAGACACC 361
Db 677 AGTGTAGAGAACTACACAGTTCTTCTGCGGTGAGATTCAATATGAGATCGAAGACACC 618
Qy 362 GGCATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 421
Db 617 GGAATTTAGGCGCGGATTCATCAAGTTCGCGACCAAGCGAGGCGACCCCTTTTCAAGAG 558
Qy 422 CTGCTCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 481
Db 557 TTAGTGTAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 498
Qy 482 ACCGCGCGCTCCGAGCGGAGCGGAGAGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 541
Db 497 ACGGAGAGAGTCAAGCGAGTGTAGAGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 438
Qy 542 TCCCGTCCGCGGTGTGATCGGCGCACTCCGAGCAGACCGAGCAGCTCTCTACCTCAC 601
Db 437 AGCCCTCAACGGGTTTGTATGTGTCAAGCGATGATATCTAGAGATTGAGCTATCTCAC 378
Qy 602 GCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 661
Db 377 GCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 318
Qy 662 CTCAGAGCAAGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 721
Db 317 CTAGAGAGTAATGTCAAGTGCATCAGCCCTCTCGGCGCGCGCGCGCGCGCGCGCG 258
Qy 722 CTCTCATCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 781
Db 257 CTCTTGAATCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 198
Qy 782 TGGCTCTTGGCGCTTCTCTCTCACTGACCAACATCATGAGCGTGTGAGCGCGGTGAC 841
Db 197 TGGCTGTTCGGGTTTTTCAGCTATGTCAACCAATCATGAGCGTGTGAGCGCGGTGAC 138
Qy 842 CCGGACGCGCATGGCGCTTCATCCGCGTCCGCGGATCCCGGTTCTCCGCGAGAGGCG 901
Db 137 CCGGACGCGAGTGGCGCTTCATTCCTGAGAGTGTCCATTCCTACGAGAGAGGCGGTG 78
Qy 902 CCGGAGAGAGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 961
Db 77 CCAAGAGAAAGCGTGTGAGGAGTCACTGTGACTAACCGCGCGGTTCTTGTCAACGAGC 18
Qy 962 CTCGCGCGCTCTCTGA 976
Db 17 TTGCGGCGGTGATGA 3

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RESULT 5  
US-10-477-469-6

; Sequence 6, Application US/10477469  
; Publication No. US20040161818A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Irene  
; APPLICANT: Sutherland, Tara

```

; APPLICANT: Harcourt, Rebecca
; APPLICANT: Russell, Robyn
; APPLICANT: Oakeshott, John
; TITLE OF INVENTION: Phosphotriesterase from Agrobacterium radiobacter P230
; FILE REFERENCE: 131-03
; CURRENT APPLICATION NUMBER: US/10/477,469
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/AU02/000594
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: AU PR 5023
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Agrobacterium radiobacter
US-10-477-469-6

Query Match      57.7%; Score 566.8; DB 18; Length 1071;
Best Local Similarity 74.0%; Pred. No. 8.8e-118;
Matches 718; Conservative 0; Mismatches 252; Indels 0; Gaps 0;

Qy 1 CCGCCCGATCCATCTCCGAGCGCGCGCTTACCCCTACCCAGACGACATCTGGGCTC 60
Db 36 CGGCCCATTCAGATTTCGAGAGCGGGGCTTCACACTGACCATGAGCATATCTCGCGGAG 95
Qy 61 CTCGCGCGCTTCTCCGCGCGCGCTGCGGAGTTCCTGCGGCTCCGCAAGGCGCTCGCGGA 120
Db 96 TTCGCGGAGATTCTTACGTGCGGTGCGGAGTTTTCGATAGCCGCAAGGCTCTAGCGGA 155
Qy 121 GAAGCGCGTGTGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 156 AAGGCTGTGAGAGATTAGCGCATGCGCAAGTGTGCGGTGCGGAAACCATGTGTGATGT 215
Qy 181 GTTCACTTGCACATCGGCGCGCGAGTGTCTCTCTGCGGAGTGTCCGCGCGCGCGGA 240
Db 216 GTTCACTTGCATATCGGTGTGAGTGTCTCTGTTTGTGCGCGAGATTTCGCGGCGCGCG 275
Qy 241 CGTGCAATGTGTGCGCGCGCGCGCTGTGTGACCGCGCGCTCTCCATGCGGCGCTCCG 300
Db 276 GTTCAATGTGTGCGCGCGCGCGCTGTGTGAGTGTGACCGCGCATTTTCATGAGTAATGCG 335
Qy 301 CTCGTGTGAGAGCTCACCCAGTTCTTCTTCCGAGATTCAGTACGAGCATGTGAGACAC 360
Db 336 CAGGTGTGAGAGATGTGACCCAGTTCTTCTGTGCGTAATTCAGATGTGAGATGTGAGACAC 395
Qy 361 CCGCATCGCGCGCGCGCATCATAGTGTGCGACCAAGCGGCAAGCGCACCCGTTCCAGGA 420
Db 396 CGGTATTAGGCGCGCGCATTTTCAAGTGTGCGACCAAGCGGAGGCGGACCCCTTTCAAGA 455
Qy 421 GCTGTGTCTCAAGCGCGCGCGCGCGCGCTCCCTGCGCACCGCGGCGGTGCGGATCACGCCA 480
Db 456 GTTGTGTATTAAAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 515
Qy 481 CACGCGCGCTCCGAGCGCGAGCGGCGAGCAGAGCGCGCATCTTCTGATGTCCGAGGCGCT 540
Db 516 CAGGTCAAGCAATGACGCGCGATGTGCGAGCAGAGGAGGAGCATATTGTAATCCGAGGTTT 575
Qy 541 CTCCTCGTTCGCGGTGTGATCGGCGCATCTCGAGAGACAGGAGCATCTTCTTACCTCAC 600
Db 576 GAGCCCTTCAGCGGTTTTGTATCGGTCAAGGAGATGTGACGATTGAGCTTACCTTAAAC 635
Qy 601 CGCCCTGCGCGCGCGCGGATTCATCGGCGGTGAGACCAATTCGCGCATTCGCGCATTCG 660
Db 636 CGGCTGTGCGCGCGCGGAGTCTCTGCGGTTTATGATGCGATGCGGATGCGGATTTGG 695
Qy 661 CTTCGAGAGCAACGCTTCGCGGTCCGCGCTCTCTCGGCGCATCGCTCTCTGAGAGACCGCGC 720
Db 696 TCTAGAGGCAATGCGAGTGTATGAGCGCTTTTGTGATCTCGGTGTGCGGCAAGAGGCG 755
Qy 721 CTCTCATCAAGGCGCTTATTCAGCGGCGTACATAGAGATCTCTGTGTCAACGA 780

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Db 756 TCTCTTGATCAAGGGCTCATCGACCGAGCTAACAGATCGAATCTCTGTCTCCCATGA 815  
Qy 781 CTGGCTCTTCGGGCTTCTCTCTACGTAGCAACATCAATGACGATGAGACCGCGTGA 840  
Db 816 CTGGCTCTTCGGGCTTCTCTCTACGTAGCAACATCAATGAGATGATGATGATGA 875  
Qy 841 CCCGAGCGGATGCGCTTCATCCCGCTCCGCGTGAATCCCGTCTCCGCGAAGAGGCGT 900  
Db 876 CCCAGATGGAATGCGCTTCGTCTCTGAGTGAATCCCATCTCTACGAGAGAGGCGGT 935  
Qy 901 GCCGAGAGAGACCTTCGCGCGGATACCGGTGACCAACCGCGCGCTCTCTCCCGAC 960  
Db 936 CCCGCGGAGAAACGTACGAGGCGTAAACGTGCGCAATCCCGCGGTTCTGTCAACGAC 995  
Qy 961 CCTCGCGGCGC 970  
Db 996 GTGCGGCGC 1005

## RESULT 6

US-10-477-469-5  
; Sequence 5, Application US/10477469  
; Publication No. US20040161818A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Irene  
; APPLICANT: Sutherland, Tara  
; APPLICANT: Harcourt, Rebecca  
; APPLICANT: Russell, Robyn  
; APPLICANT: Oakeshott, John  
; TITLE OF INVENTION: Phosphotriesterase from *Agrobacterium radiobacter* P230  
; FILE REFERENCE: 131-03  
; CURRENT FILING DATE: 2003-11-12  
; PRIOR FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: PCT/AU02/000594  
; PRIOR FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: AU PR 5023  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 1155  
; TYPE: DNA  
; ORGANISM: *Agrobacterium radiobacter*  
US-10-477-469-5

Query Match 57.7%; Score 566.8; DB 18; Length 1155;  
Best Local Similarity 74.0%; Pred. No. 8,8e-118;  
Matches 718; Conservative 0; Mismatches 252; Indels 0; Gaps 0;

Qy 1 CGGCGGATCAACATCTCCGAGCGCGGCTTCAACCTCAACCCGACGACATCTGGGCTC 60  
Db 120 CGGCGGATCTCAAGTTTGGAGCGGCTTCAACCTCAACCCGACGACATCTGGGCTC 179  
Qy 61 CTCCGCGGCTTCTCTCCGCGCTGCGCGAGTTCTTTCGCTCCCGCAAGGCGCTTCGCGA 120  
Db 180 TTCCGCGGAGATTCTTACGTCGTCGCGAGTTTTCGCTTACCGCAAGCTCTAGCGGA 239  
Qy 121 GAAAGCGTGGCGGCTTCG 180  
Db 240 AAAAGCTGTGAGAGATTACCGCATGCGAGATCGGCTGCGCAAAACCATCTGTGATGT 299  
Qy 181 GTCCACTTTCGACATCG 240  
Db 300 GTCCACTTTCGACATCG 359  
Qy 241 CGTGACATCTGTGCG 300  
Db 360 CGTGACATCTGTGCG 419  
Qy 301 CTCGCTGAGAGACATCCCAAGTTTCTCTCCGCGAGATCCGATCCGATGAGAGAC 360  
Db 420 CAGCTGAGAGACATCCCAAGTTTCTCTCCGCGAGATCCGATGAGAGAC 479

Qy 361 CGGATCCGCGCGCGCATCATCAAGTGGCCACCAACCGGACAGCAACCCGTTCCAGGA 420  
Db 480 CGGATTAAGGCGGCGCATTAATCAAGTGGCCACCAACCGGAGAGGCGAGCCCTTTCAAGA 539  
Qy 421 GCTGTGCTCAAGGCG 480  
Db 540 GTTGTGTTAAAGGCGAGCG 599  
Qy 481 CACGCGCGCTCCGAGCG 540  
Db 600 CACGTACAGAGTACG 659  
Qy 541 CTCCCGCTCCG 600  
Db 660 GAGCCCTCACGCGGTTTGTATGGTCAAGGATGATCTGACGATTTGAGCTTACCTAAC 719  
Qy 601 CGCCCTGCG 660  
Db 720 CGGCTTCGCTCG 779  
Qy 661 CCTGAGAGCAAGCGCTCCG 720  
Db 780 TCTAGAGGCAATGCGAGTGAATTAAGCTTTTGTATCTCGTGTGGCAAAACAGGCG 839  
Qy 721 CTCTCTCATCAAGGCGCGCGCATCGACCAAGGCTTACATGAGAGATCTCTGTCCAAAG 780  
Db 840 TCTCTTGATCAAGGCGCGCGCATCGACCGAGGCTTACATGAGATCTCTGTCCAAAG 899  
Qy 781 CTGGCTCTTCGGGCTTCTCTCTTACGTGACCAACATCAATGAGATGAGACCGCGTGA 840  
Db 900 CTGGCTCTTCGGGCTTCTCTCTTACGTGACCAACATCAATGAGATGAGATGAGATGAA 959  
Qy 841 CCCGAGCGGATGCGCTTCATCCCGCTCCGCGGTATCCCGTCTCCGCGAAGAGGCGT 900  
Db 960 CCCGAGGAAATGCGCTTCGCTCTGAGATGATCCCATTTCTTCAAGAGAGAGGCGT 1019  
Qy 901 GCCGAGAGACCTTCGCGCGCATCACCGGTGACCAACCGCGCGCGCTTCTCTCCCGAC 960  
Db 1020 CCCGCGGAAAGCTGAGAGGCGTAAACCGTGGCAATCCCGCGGCTTCTGTACGAC 1079  
Qy 961 CCTCGCGCGC 970  
Db 1080 GTGCGGCGC 1089

## RESULT 7

US-10-477-469-8  
; Sequence 8, Application US/10477469  
; Publication No. US20040161818A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Irene  
; APPLICANT: Sutherland, Tara  
; APPLICANT: Harcourt, Rebecca  
; APPLICANT: Russell, Robyn  
; APPLICANT: Oakeshott, John  
; TITLE OF INVENTION: Phosphotriesterase from *Agrobacterium radiobacter* P230  
; FILE REFERENCE: 131-03  
; CURRENT FILING DATE: 2003-11-12  
; PRIOR FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: PCT/AU02/000594  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 1155  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE: Mutant of Opda  
US-10-477-469-8

Query Match	57.6%	Score 565.2;	DB 18;	Length 1155;
Best Local Similarity	73.9%	Pred. No. 2e-117;		
Matches 717; Conservative	0;	Mismatches 253;	Indels 0;	Gaps 0;

Qy		CGGCCCCATATCAATCTCCGAGGCGGGCTTCAACCTCCACCCAGAGCAATCTGGGGCTC	60
Db	120	CGGCCCCATTCAGATTTCGGAAACGGGGCTTTCACACTGACCCATGAGCATATCTGGGGCAG	179
Qy	61	CTCCGCGGGCTTCTCTCCGCGCCCTGGCCGGAGTTCCTTCGGCTTCCCGCAAGGCCCTCGCCGA	120
Db	180	TTCCGCGGGGATTCCTAACGAGCGGTGGCCGGAGTTCCTTCGGTACCGCCAAAGCTCTAAGCGGA	239
Qy	121	GAAGGCCGTGGCGGGCTTCGCCGGCGCCCGCCGCGCGCTGGCTGGCACCATTGTGGAGGT	180
Db	240	AAAGGCTGTGAGAGGATTAACGCATGCAAGATCGGCTGGCGTGCAGAAACCATGTCGATGT	299
Qy	181	GTCCACTTTCGACATTCGGCGCGGACGCTGACCTCTCCGCGCAGAGTGTCGCCGCGCGCCGA	240
Db	300	GTCCACTTTCGATATTCGGTCTGTGACGTCCGTTTATTTGGCCGAAGTTTGGCGGGCCGACGA	359
Qy	241	CGTGCACATCGTGGCGCGGACCCGGACCTCTGTTCGACCCGCGCTCTCCATGCGCTCG	300
Db	360	CGTGCATATCGTGGCGGGGACGAGCTGAGTTATGTTTGCACCGGCCACTTTCAAATGCAATGG	419
Qy	301	CTCCGTGAGAGCTCACCCAGTTCTTCTCTCGCGAGATCCAGTACGGCATTGAGAGACAC	360
Db	420	CAGCCTCCAAAGACTGACCCAGATTCTTCTGTGTAAATCCAACTGGCATGGAAGACAC	479
Qy	361	CGGCATCCGCGCGCGGCATCATCAAGTGGCCACACCGGCAAGGCGCACCCGTTCCAGGA	420
Db	480	CGGTTTATGGCGGGCATTTATCAGGTGCGACACCAAGGAAAGGCGACCCCTTTCAAAGA	539
Qy	421	GCTCGTGCTCAAAGCGCGCGCGCGCTCTCTCGCCACCGGCGTGGCGGTGACCAACCA	480
Db	540	GTTGGTGTAAAGGCGAGCGCGCGGGCCAGCTTGGCCACCGGTGTTCGGTAAACCATCA	599
Qy	481	CACGCGCCCTCTCCAGCGCGGACAGGAGACAGAGAGCCGCGCATCTTCGAGTCCGAGGGCT	540
Db	600	CACGTCAACAAAGTCAAGCGGATGGGAGACAGAGGACAGCCAAATTTGAAATCGAAGGTTT	659
Qy	541	CTCCCGCTCCGCGGTGTCATCGGCGCATCCGACGACACCGACGACCTCTCCTACCTCAG	600
Db	660	GAGCCCTTCACGGGTTTGTATCGGTCAACAGCATGATATGACGATTTGAGTACTTAAC	719
Qy	601	CGCCTCGCCCGCGCGGCTACCTTCATCGGCTCGACCAATCCGCGCACTCCGCGCATCGG	660
Db	720	CGGCTCTCGCTCGCGCGGATACCTGTGAGTTAATGCGATGCGTACAGTGCAGATTGG	779
Qy	661	CCTGAGGACAAAGGCTCGCGGTCCGCGCTCTCGGCGATCGGCTCTGTGACAGACCCGGCG	720
Db	780	TCGTAAAGGACATGAGGTGACTTAAAGCCTCTTGTGTACTCGGTGTGGCAAAAGGAGC	839
Qy	721	CCTCCTCATCAAGGCCCTCATGACCAAGGCTACATGGAAGCATCTCGTGTCAACGA	780
Db	840	TCTCTGATCAAGGGGCTCATGACCGAGGCTACAAAGATCGAATCTCTGTCTCCCACTGA	899
Qy	781	CTGAGCTCTCGGCTTCTCTCTTACGTGACCAACATCATGACGTGATGAGCCGGGTAA	840
Db	900	CTGAGCTGTTCGGGTTTTCGAGCTATGTACAGAACATCATGACGTAAATGAGATCGCATAA	959
Qy	841	CCCGGACGGCATAGGCTTCATCCGCGCTCCGCGTATCCCGTTCTCCCGGAGAAAGGGGT	900
Db	960	CCCGATGAATAGGCTTCGTCTCTGTAGAGTATCCCATTCCTACAGAGAAAGGGGT	1019
Qy	901	GCCGAGAGAGACCTTCGCGCGGCATCACGATGACCAACCGCGCGCGCTTCTCTCCCGAC	960
Db	1020	CCCGCGGAAACGCTAAGAGGGGTAAACGTGGCCAAATCCCGGGGTTCTTGTCAACGAC	1079
Qy	961	CCTCGCGGCC	970
Db	1080	CGTGGCGGCC	1089

```

RESULT 8
US-10-477-469-7
; Sequence 7, Application US/10477469
; Publication No. US20040161818A1
GENERAL INFORMATION:
APPLICANT: Horne, Irene
APPLICANT: Sutherland, Tara
APPLICANT: Harcourt, Rebecca
APPLICANT: Russell, Robyn
APPLICANT: Oakeshott, John
TITLE OF INVENTION: Phosphotriesterase from Agrobacterium radiobacter P230
FILE REFERENCE: 131-03
CURRENT APPLICATION NUMBER: US/10/477, 469
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/AU02/000594
PRIOR FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: AU PR 5023
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Mutant of Opda
US-10-477-469-7

```

Query Match	Similarity	57.2%	Score 562;	DB 18;	Length 1155;	
Best Local	Similarity	73.7%	Pred. No. 1e-116;			
Matches	715;	Conservative	0;	Mismatches 255;	Indels 0; Gaps 0	
Qy	1	CGGCGCGATCAACATCTCCGAGGCCGGCTTCA	CCCTCA	CCCAAGACGACATCTGGGCTC	60	
Dp	120	CGGCTTCATTCAGATTTCGGAAGCGGGCTTCA	CTGAC	CTGACCCATGAGCATATCTGCGGCAG	179	
Qy	61	CTCGCGCGGCTTCTCCGCGGCTTGCCGGA	GTTC	CTTCGGCTCCGCGAAGCCCTCGGCGA	120	
Dp	180	TTTCGGCGGGAATTCACGCTGCGTGGCCG	GAAGTTTTCGGTAC	CCGCAAAAGCTCTGACGGA	239	
Qy	121	GAAGGCGTGGCGGGCTCTCCGCGGGCCG	CGCGCGCGAGTGC	CGACCACTGTGGACGT	180	
Dp	240	AAAGGCTGTGAGAGGATTAACGCGATCC	CAAGATCGGCTGG	CGTGCAAAACATGTGATGT	299	
Qy	181	GTCCACCTTCGACATCGGCGCGGACGTG	TCCCTCTCTCG	CGAGGTGTCCGCGCGCGCGA	240	
Dp	300	GTGCACTTTCATATACGGTGTGACGTCCG	TTATTATGGCGGA	AGTTTCCGCGGCGCGCGA	359	
Qy	241	CGTGACATCGTGGCGCGGACCGGCGCTC	MGTTTGAC	CGCGCGCGCTCTGCATCGGCTCG	300	
Dp	360	CGTGCAATTCGTGGCGGCGACTGGCTT	TATGGTTCA	ACCCGCTTCACTTTCATGTGCAATGG	419	
Qy	301	CTCGGTGAGAGCTCAACCGATTCTTCTC	CCCGAGATTC	CAAGTACGCGCATCGAGGAC	360	
Dp	420	CAGCGTCGAAGAATCGACCCAGATTCTT	CTGTGGTGA	AAATCCAAATGGCATCGAAGAC	479	
Qy	361	CGGCAATCCGCGCCCGGCATATCAAGT	TGGCCAC	CCGCGCAAGGCCACCCCGTTCAGGA	420	
Dp	480	CGGATTTAGGGCGGGCATTTATCMAAGT	CTCGAC	CCACAGGGAAGGGACCCCTTTCMAA	539	
Qy	421	GCTCGTGTCAAGGCGCGCCCGCGGCTCT	CCCTCCCA	CCGAGTGC	CGGTACCA	480
Dp	540	GTTGGGTGTTAAAGGAGGCGCGCGGGC	AGCTTGGCC	ACACGGGTCTTCGGGTAA	599	
Qy	481	CACCGCGGCTTCCACGCGCGAGCGAG	AGAGAGGCGCGCATCTT	CGAGTCCGAGGGCCT	540	
Dp	600	CACGTCAACAAGTCAGCCCGATGGG	AGACAGAGGACAGCAATTTG	AATCCGAAGGTTT	659	
Qy	541	CTCCCGGTCGCGCGGTGATCGGCACT	CGGACGA	CCGACGACTTCCTACCTCAG	600	
Dp	660	GAGCCCTTCACGGGTTTGTATCGGT	CAACAGCATATATCGA	ATTGGGCTTACCTTAAC	719	
Qy	601	CGCCCTCGCGCGCGCGGCTACTTAT	CGGCTCGAC	CAACATCCGCACTCCGCAATCG	660	

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Db      720 CGGCTCGCTGCGCGCGGATACCTCGTGGTTAGATGCATGCCGTACAGTGCATTTGG 779
Qy      661 CCTGAGAGCAACGCTCCGCGTCCGCTCTCTGCGGATCCGCTCTCTGAGAGACCCGCGC 720
Db      780 TCTGAAAGGCAATCGAGTGCATTAGCGCTCTTGGTCTCGTGTGGCAAAACAAGGGC 839
Qy      721 CCTCTCATCAAGGCGCTCATGCAGCAGGCGCTACATGAAGAGATCCTCGTCCAAAGA 780
Db      840 TCTCTTATCAAGGCGCTCATGCAGCAGGCGCTACATGAAGATGCAATCTCTCTCCATGA 899
Qy      781 CTGCTCTTCCGCTTCTCTCTCTCTACGTAGCAACATCATGACGTATGACCCGCTGA 840
Db      900 CTGGCTGTTGGGTTTTCAGACTATGTCACGAACATCATGACGTATGACATGCAATAA 959
Qy      841 CCCGACGGCATGCGCTTCTCATCCGCTCCGCGTATCCGCTCTCTCCGAGAAAGGCGT 900
Db      960 CCCAGATGGAATGGCGCTTCTCTCTCTCTGAGTGTATCCCATTTCTACGAGAAAGGCGT 1019
Qy      901 GCCGACGAGAACCTCGCGCGCATCACCGTACCAACCCGCGCTCTCTCCCGAGC 960
Db      1020 CCCGCGGAAACCTAGACAGGCGTAAACCGTGCATCCCGCGCTTCTGTCAACGAC 1079
Qy      961 CCTCGCGCC 970
Db      1080 CGTGGCGCC 1089

```

# RESULT 9 US-10-282-122A-25658

Sequence 25658, Application US/10282122A  
Publication No. US20040029129A1

## GENERAL INFORMATION:

APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

PRIOR FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: Patent version 3.1  
SEQ ID NO 25658

LENGTH: 978  
TYPE: DNA  
ORGANISM: Mycobacterium avium  
US-10-282-122A-25658

Query Match 17.0%; Score 167.4; DB 17; Length 978;  
Best Local Similarity 51.2%; Pred. No. 2.3e-28;  
Matches 467; Conservative 0; Mismatches 416; Indels 30; Gaps 2;

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Qy      1 CGGCCCATATCATCTCCGAGCGCGCTTACCCCTACCCAGAGCATCTGCGGCTC 60
Db      24 CGGCGCCATTCACACCGCTGCGCTGGGTGTACCTGATGACAAACGTTTCATAT 83
Qy      61 CTCGCGGCTTCTCTCCGCGCTGCGGAGTTCTTCCGCTCCGCAAGCCCTGCGCA 120
Db      84 GATCACAAGATCCCGAGAACTACCCGAAAGCGTGGGCGACGAAGAGCGGGTGGC 143
Qy      121 GAAGCGCTGCGCGGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 180
Db      144 CGAGCCCATTCAGCCGCTCAACGAGCTCAAGGCGCGCGCGCTGAGACACATCTG 203
Qy      181 GTCCACCTTCGACATCCGCGCGCGCGCGCTGCTCCCTCGCGCGAGGTGTCGCG 240
Db      204 CACGTCATTCGACCTGCGCGCTGCTACATTCGCGGATCGCGGATCGCGCGCA 263
Qy      241 CGTGCATCTGTCGCGCGCGCGCGCTGCTGCTGACCCGCGCTTCTCATGCGCTCG 300
Db      264 GCTGAATATCTGTGTGGCAAGGGGCTTTACACCTACGAAGATGTCCTTATTTCA 323
Qy      301 CTCGCT-----GAGAGCTCACCCAGTTCTTCTCTCG 333
Db      324 CTACCTGGGCGCGGCGCGAGCTGAGCGCGCGCGCGCGCATGACCGCATGTTCTG 383
Qy      334 CGAATTCAGTACCGCATTCAGAGCAACCGGATCCGCGCGCGCATCATAGTGGCCAC 393
Db      384 CGACATTCAGAGGAGCATTCGCGACACCGGATCAAGGCGCGCATCTCAATGCGCAC 443
Qy      394 ---CACCGCAAGGCAACCCGTTCCAGAGCTGCTCAAGGCGCGCGCGCGCTC 450
Db      444 TGACGACCCGCGCTGCTCCGCGGTGAGAGCGGTGCTGGGCGGTGGCGCAAGCGCA 503
Qy      451 CCTCGCACCGGCGGTGCGGTGACCAACCGCGCGCTTCCAGCGCGAGCGAGCA 510
Db      504 CAAGCGCACCGGCGGTGCGGTGCTCCACGACACCCAGCGCGGTGCGCGCGCTCGA 563
Qy      511 GCGGCGCGCATCTTCTGAGTCCGAGGCGCTTCCCGCTCCGCGGTGATCGGCACTC 570
Db      564 CCGAGCGGAGATCTTCCGAGAGAGGCGGTGACCTGAGCGCGGTGATCGGCACTC 623
Qy      571 CGAGGACCGAGCACTCTCTTACCTCACCGCGCTGCGCGCGCGCTACCTCATCGG 630
Db      624 CGGCAACGACCGAGCTGCGGTACTGAGAGCTCATCGCGCGCTCATATCTGGG 683
Qy      631 CCTCGACCATCCCGCATCCGCACTCCGCGCTGAGAGCAAGCTTCCGCGCTCGCCT 690
Db      684 CATGACCGGTTCGCGATTCAGACGATCTCCGCGTTCCAGAGCGGATGAAATGTCG 743
Qy      691 CTTGCGCATCCGCTCTGCGAAGACCGCGCGCTCTCTCATCAAGGCGCTCATGAC 750
Db      744 GCGATGTCGAGCGCGCGCACGCGCAAGATGTGCTCTGCAAGAGCGCAACTGTTA 803
Qy      751 CTACATGAAGCAGATCTCTGTCCACGACTGAGCTTTCGCTTCTCTCTTACGTGAC 810
Db      804 TTTCCAGCAGCTTCCCGAGAGTGTGTGCCCCAGATCATGCGAACTGACATTACTG 863
Qy      811 CAACATCATGACGTGATGAGCCGCGTGAACCGGACCGGATGCGCTTATCTCCGCTCG 870
Db      864 CATTCACAAAGAGTGTATCCCGCTCAAGAGCGCGCGTCCAGCAAGCAACTGCA 923
Qy      871 CGTATCCGCTTC 883
Db      924 CACCATGCTGCTC 936

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RESULT 10
US-10-282-122A-28172
; Sequence 28172, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28172
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-28172

Query Match      16.9%; Score 166.4; DB 17; Length 981;
Best Local Similarity 55.5%; Pred. No. 3.8e-28;
Matches 382; Conservative 0; Mismatches 276; Indels 30; Gaps 2;

QY      1 CGGCCCCATCACCATCTCCGAGCGCGGCTTCACTCCACCGACGACATCTGGCGCTC 60
DB      24 CGGAGCCCATCGACACCGCTGATCTCGGCGTACGCTGATGACGACGACGCTTTCATCAT 83
QY      61 CTCGCGCGGCTTCTCCGCGCGCTGCGCGGAGTCTTCGCGCTCCGCGGAGGCGCTCGCGCA 120
DB      84 GACCAACCGAGATGGCGGAACTACCGGAGGCTGGGGCGACGAGACAGGCGGCGG 143
QY      121 GAAGCGCGTGGCGGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB      144 CGGCGCGCATCGCGCGGCTAGGAGAACTCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 203
QY      181 GTTCACTTTCGACATCGCGCGCGGACGCTGCTCTCTCGCGAGGCTGTCGCGCGCGCG 240
DB      204 CACGCTGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 263
QY      241 CGTGACATCGTGGCGCGCGCGCGCGCGCTGCTGATGACCGCGCGCTCTCATGCGCTCG 300
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DB      264 GCTGAACATCGTCTGCGCACCGGCTTGTAACCTTACACGACGTCCTCCCTTACTTCCA 323
QY      301 CTCGCT-----GGAGAGCTCAACCCAGTTCTTCTCCG 333
DB      324 CTACCTCGGGCGGGCGGACAGCTGAGCGGCCGAGATCATGACCGACATGTTCTGTCG 383
QY      334 CGAGATTCAGTACGGCATCGAGACATCGGCATCCGCGCGCGCATCATCAAGTGGCCAC 393
DB      384 CGACATTCAGACGCGCATCGCGACACCGGCATCAAGCGGGAATCTCTCAAGTGGCCAC 443
QY      394 CACCGCAAGGCG---CACCGCTTCAGGAGCTGTGCTCAAGGCGCGCGCGCGCTC 450
DB      444 CGACCAACCCGCGCTCACCTCTGCTGAGCGGCTGTGGCGCGCTTCAAGCA 503
QY      451 CTCGCGCACCGCGCTGCGGTGACCAACCAACCGCGCTCCGACCGCGAGCGAGCA 510
DB      504 CAACGACACCGGGGGCGGATCTCCACCAACCGCGCGGGGTGGCGCGCGCTTGA 563
QY      511 GAGGCGCGCATTTTTCAGTCCGAGGCTCTCCCGCTCCGCGTGTGATCGGCATC 570
DB      564 CAGCAACGCAATCTTCGCGCGAGGAGGCTGACCTGAGCGGCTGTTATCGACACTG 623
QY      571 CGAGCACACGACGACCTCTCTACTTCAACCGCGCGCGCGCGCTACTTCATCG 630
DB      624 CGGCAACGACACGACGCTGCTGCTTACTTGAAGACTCATCGCGCGCTCTTACTCG 683
QY      631 CCTGACCAATCCCGCACTCCGCATC 658
DB      684 GATGACCGGTTTCGCGCTGACGATGATC 711
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RESULT 11
US-10-282-122A-26226
; Sequence 26226, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
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NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: Patent in version 3.1  
SEQ ID NO: 26226  
LENGTH: 918  
TYPE: DNA  
ORGANISM: Mycobacterium bovis  
US-10-282-122A-26226

Query Match 15.2%; Score 148.8; DB 17; Length 918;  
Best Local Similarity 54.9%; Pred. No. 3.3e-24;  
Matches 356; Conservative 0; Mismatches 262; Indels 30; Gaps 2;

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QY 41 CACGACATCTGCGCTCTCCGCGGCTTCTCCGCGCTGCGCGAGTTCTTCGCG 100
DB 4 CACGACATCTTCTTATGATGACCAAGATTGGGCAAGACTACCGGAAGCTGGGCG 63
QY 101 TCCCGCAAGCCCTGCGCGAAGGCGGCTGCGGCGCTCCGCGCGCGCGCGCGCG 160
DB 64 GACGAGGACAGCGGCTGCGCGGCTGCGCGCTGCGCGGAACTCAAGGCGCGCGCG 123
QY 161 GTCGACCATCTGCGGAGCTGTCACCTTCCGACATCGCGCGGAGGCTGCTCCGCGCG 220
DB 124 GTGACACATCTGCGCTCAAGGATGATCGGCGGCGGCGGATGATCCGCGCATGCGC 183
QY 221 GAGGTGTCGCGCGCGCGCGCGCGCATGATGATGCGCGCGCGCGCTGTTGACCGCG 280
DB 184 CGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 243
QY 281 CGGCTGTCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 313
DB 244 GACGTCGCGCTTCTACTTCCATCTACCTCGGCGCGCGCGCGCGCGCGCGCGCGCG 303
QY 314 CTCACCGAGTTCTTCTCCGCGAGATTCAGTACGATGATGAGACACCGCGCATCGCGCG 373
DB 304 ATGACCGAGATCTTGTCTCGCGACATCGAGCAAGGATGCGCGCGCGCGCGCGCGCG 363
QY 374 GGCATCTATCAAGTGGCGCAACCGCGCAAGGCGCGCGCGCGCGCGCGCGCGCGCG 430
DB 364 GGAATCTCTAATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 423
QY 431 AAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 490
DB 424 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 483
QY 491 TCCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 550
DB 484 GGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 543
QY 551 CGCGGTGCGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 610
DB 544 CGGCTGCTTATGGACACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 603
QY 611 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 658
DB 604 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 651
```

RESULT 12  
US-10-363-345A-31407/c  
Sequence 31407, Application US/10363345A  
Publication No. US20040234960A1  
GENERAL INFORMATION:  
APPLICANT: Alexander Olek  
APPLICANT: Christian Piepenbrock  
APPLICANT: Kurt Berlin  
TITLE OF INVENTION: Method for determining the degree of methylation of defined  
FILE REFERENCE: E01/1227  
CURRENT APPLICATION NUMBER: US/10/363,345A  
NUMBER OF SEQ ID NOS: 2003-03-03  
SEQUENCE OF SEQ ID NOS: 40712  
LENGTH: 985

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
OTHER INFORMATION: Cpg-Island No: 31407  
US-10-363-345A-31407

Query Match 13.9%; Score 136.2; DB 18; Length 985;  
Best Local Similarity 47.9%; Pred. No. 2.2e-21;  
Matches 428; Conservative 0; Mismatches 458; Indels 7; Gaps 1;

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QY 1 CCGCCGATTCACCATCTCCGAGCGCGGCTTCAACCTCAACCCAGACGACATCTGCGCTC 60
DB 984 CGTCGACATCGACATCTACATCTACGTCTACATCTACGTCACGTCGACATCGACATCA 925
QY 61 CTCGCGCGGCTTCTCCGCGCGCTGCGCGGAGTTCTTCGCGCTCCGCGAGGCGCTGCGCA 120
DB 924 CATCTACGTGACATCTACGTGACCTGACATCTACGTGACATCTACGTGACATCTAC 865
QY 121 GAAAGCGCGCGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 864 CGTCGACATCGACATCTACGTGACCTGACCTGACATCGACGTGACATCGACGTGAC 805
QY 181 GTTCACCTTGCACATCGCGCGCGCGCGCGCTTCTCCGCGAGGCTGTCGCGCGCGCGCA 240
DB 804 CCGTCGACGTGACATCGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGAC 745
QY 241 CGTGCACA-----TCGTGCGCGCGCGCGCGCGCTGCTGCTGCGACCGCGCGCTTCGATGC 293
DB 744 CATCTACGATTCACGTCGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGAC 685
QY 294 GCGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 353
DB 684 ACATCTACGTGACATCTACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGAC 625
QY 354 AGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 413
DB 624 AGTGAAGGTGACATCTACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGAC 565
QY 414 TCCAGAGGTGCTGCTCAAGGCGCGCGCGCGCGCGCTTCTCCGCGCGCGCGCGCGCG 473
DB 564 ACATGAGGTGACATCTACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGAC 505
QY 474 CCACCGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 533
DB 504 ACCTTACATCAACATCAACATCTACATCTACATCTACATCTACATCTACATCTACATCT 445
QY 534 AGGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 593
DB 444 ACATCTACGTGACATCTACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGAC 385
QY 594 ACCTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 653
DB 384 ACCTGACATCTACGTGACATCTACGTGACATCTACGTGACATCTACGTGACATCTACGT 325
QY 654 CCATGCGCTGAGGACAAAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 713
DB 324 ACATCTACGTGACATCTACGTGACATCTACGTGACATCTACGTGACATCTACGTGAC 265
QY 714 CCGCGCGCGCTTCTCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 773
DB 264 ACCTGACATCTACGTGACATCTACGTGACATCTACGTGACATCTACGTGACATCTACGT 205
QY 774 CCAAGACTGCGCTTTCGCGCTTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 833
DB 204 ACCTGACATCTACGTGACATCTACGTGACATCTACGTGACATCTACGTGACATCTACGT 145
QY 834 GGTGAACCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 886
DB 144 ACATCTACGTGACATCTACGTGACATCTACGTGACATCTACGTGACATCTACGTGAC 92
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RESULT 13





QY 484 CGCGCTCCGACGCGGACGAGCCGCCATCTTGAGTCCGAGGCTCTTC 543  
 Db 666 CGGCATCCGCATCCGCATCGGCGTGGGATCCGCATCTGCATCGGCGTACGATCCGCAT 607  
 QY 544 CCGGCTCCGCGTGGGATCGGCACTCCGACGACCGACGACTCTCTCACTCAAGCC 603  
 Db 606 CGGCGTCAGCATCCGCATCCGCATCGGCGTCCGCATCCGCATCCGCATCCGCAT 547  
 QY 604 CCGCGCGCGCGGCTCACTCACTCGGCTCGACCAATCCGCACTCCGCACTCGGCT 663  
 Db 546 CTGCATCGGCGTCAAGCTCAAGCTCAAGCTCGGCGTCAAGCTCAAGCTCAAGCT 487  
 QY 664 CGAGCAACGCGCTCCGCGTCCGCTCTCGGCAATCCGCTCTCGGCAACCCGCGCT 723  
 Db 486 CGGCATCCGCATCTGCATCGGCGTCAAGCTCAAGCTCGGCGTCAAGCTCAAGCT 427  
 QY 724 CCGTCAAGGCGCTCACTCACTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGG 783  
 Db 426 CGGCGTCAGCATCCGCATCCGCATCGGCGTCCGCATCCGCATCCGCATCCGCAT 367  
 QY 784 GCTCTCGGCTTCTCTCTCACTCACTCAAGCAATCAAGCAATCAAGCAATCAAGCA 843  
 Db 366 CGGCATCCGCATCCGCATCGGCGTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCT 307  
 QY 844 GAGCGCATGCGCTTCACTCCGCTCCGCT--GATCCGTTCTCCGAGAGAGGCT 900  
 Db 306 CGGCGTCAGCATCCGCATCCGCATCGGCGTCAAGCTCAAGCTCGGCGTCAAGCT 247  
 QY 901 GCGCGAGAGACCTTCGCGGATCAAGCTCAAGCAACCGCGCTTCTCTCCCGAC 960  
 Db 246 CGGCGTCAGCATCCGCATCCGCATCGGCGTCAAGCTCAAGCTCCGCATCCGCAT 187  
 QY 961 C 961  
 Db 186 C 186

RESULT 15  
 US-10-398-221-613  
 ; Sequence 613, Application US/10398221  
 ; Publication No. US20040018514A1

; GENERAL INFORMATION:  
 ; APPLICANT: KUNST, Frederik  
 ; APPLICANT: GLASER, Philippe  
 ; TITLE OF INVENTION: Listeria innocua, genome and applications  
 ; FILE REFERENCE: 344 702 - US  
 ; CURRENT APPLICATION NUMBER: US/10/398,221  
 ; PRIOR FILING DATE: 2003-03-27  
 ; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061  
 ; PRIOR FILING DATE: 2001-10-04  
 ; PRIOR APPLICATION NUMBER: FR 00/12 697  
 ; NUMBER OF SEQ ID NOS: 4025  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 613  
 ; LENGTH: 1311  
 ; TYPE: DNA  
 ; ORGANISM: Listeria innocua  
 US-10-398-221-613

Query Match 12.5%; Score 122.6; DB 17; Length 1311;  
 Best Local Similarity 46.2%; Pred. No. 2,4e-18;  
 Matches 444; Conservative 0; Mismatches 514; Indels 3; Gaps 1;

QY 4 CCGCATCACTCTCGAGGCGGCTTACCTCAACCAAGACATCTGGGCTCTTC 63  
 Db 190 CGGCATCTGCATCCGCATCGGCGTCAAGCTCAAGCTCGGCGTCAAGCTCGGCT 249  
 QY 64 CGCGGCTTCTCGGCGCTCGGCGGAGTTCTTGGGCTCCCGAAGGCGCTCGCGAGAA 123  
 Db 250 CTGCATCCGCATCTGCATCGGCGTCAAGCTCGGCGTCAAGCTCGGCGTCAAGCT 309  
 QY 124 GCGCGTGGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 183

Db 310 CCGCATCCGCATCCGCATCCGCATCGGCGTGGGATCCGCATCTGCATCGGCGTACGATCCGCAT 369  
 QY 184 CACCTTCAGATCCGCGCGGAGCGTGTCCCTCTCGCGAGGAGTGTCCGCGCGCGAGAGT 243  
 Db 370 CCGCATCAAGCTTGGCATCCGCATCCGCATCGGCGTCAAGCTCGGCGTCAAGCTCGGCGT 429  
 QY 244 GCACATCTGGCGCGCAACCGGCTCTGTGTGACCCGCGCTTCTCACTCAAGCTCGGCT 303  
 Db 430 CGGCATCGGCGTCAAGCTCCGCATCAAGCTCAAGCTCGGCGTCAAGCTCCGCATCCGCAT 489  
 QY 304 CCGGAGAGGCTCAACCAAGTTCTTCTCGGAGATCCAGTACGATCCGCATCCGCATCCGCAT 363  
 Db 490 CCGCATCAAGCTTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCT 549  
 QY 364 CATCCGCGCGGCAATCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 423  
 Db 550 CAGCGTCCGCGTCCGCATCCGCATCGGCGTCAAGCTCCGCATCCGCATCCGCATCCGCAT 609  
 QY 424 CCGTCAAGGCGCGCGCGCGCTCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 483  
 Db 610 CCGCATCTGCATCCGCGTGGGATCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCT 669  
 QY 484 CGCGCTCCGACGCGGACGCGGAGACGAGCGGCGCATCTTCAAGTCCGAGGCTCTTC 543  
 Db 670 CCGCATCCGCATCCGCATCCGCATCGGCGTCAAGCTCAAGCTCGGCGTCAAGCTCGGAT 729  
 QY 544 CCGGCTCCGCGTGGGATCCGCATCCGCATCGGCGTCAAGCTCAAGCTCGGCGTCAAGCT 603  
 Db 730 CGGCGTCAGCATCCGCATCCGCATCGGCGTCAAGCTCCGCATCCGCATCCGCATCCGCAT 789  
 QY 604 CCGCGCGCGCGGCTCACTCACTCAAGCAATCAAGCAATCAAGCAATCAAGCAATCAAGCA 663  
 Db 790 CTGCATCCGCATCCGCATCGGCGTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCT 849  
 QY 664 CGAGCAACGCGCTTCGCGTCCGCTCTCTGGGATCCGCTCTCGGAGAGCCGCGCT 723  
 Db 850 CCGCATCCGCATCTGCATCCGCATCGGCGTCAAGCTCGGCGTCAAGCTCCGCATCCGCAT 909  
 QY 724 CCGTCAAGGCGCTCACTCACTCAAGCAATCAAGCAATCAAGCAATCAAGCAATCAAGCA 783  
 Db 910 CGGCGTCAGCATCCGCATCCGCATCGGCGTCAAGCTCCGCATCCGCATCCGCATCCGCAT 969  
 QY 784 GCTCTCGGCTTCTCTCTCACTCACTCAAGCAATCAAGCAATCAAGCAATCAAGCAATCAAGCA 843  
 Db 970 CGGCATCCGCATCCGCATCGGCGTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCT 1029  
 QY 844 GAGCGCATGCGCTTCACTCCGCTCCGCT--GATCCGTTCTCCGAGAGAGGCGCT 900  
 Db 1030 CGGCGTCAGCATCCGCATCCGCATCGGCGTCAAGCTCCGCATCCGCATCCGCATCCGCAT 1089  
 QY 901 GCGCGAGAGACCTTCGCGGATCAAGCTCAAGCAACCGCGCTTCTCTCCCGAC 960  
 Db 1090 CGGCGTCAGCATCCGCATCCGCATCGGCGTCAAGCTCCGCATCCGCATCCGCATCCGCAT 1149  
 QY 961 C 961  
 Db 1150 C 1150

Search completed: February 12, 2005, 06:40:04  
 Job time : 478 secs

**THIS PAGE BLANK (USPTO)**



[illegible]

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RESULT 2
US-08-844-274-20
Sequence 20 Application US/08844274B
Patent No. 6218185
GENERAL INFORMATION:
APPLICANT: Fraser Jr., Malcom J.
APPLICANT: Shirk, Paul D.
APPLICANT: Perera, Omachthage
APPLICANT: Perera, Omachthage
TITLE OF INVENTION: Plagisync Transposon-Based Genetic Transformation System
TITLE OF INVENTION: for Insects
FILE REFERENCE: 0148.96
CURRENT APPLICATION NUMBER: US/08/844,274B
CURRENT FILING DATE: 1997-04-18
EARLIER APPLICATION NUMBER: 60/016,234
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0 - beta
SEQ ID NO 20
LENGTH: 7560

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pJEt.2hs/opd
US-08-844-274-20

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Query Match	64.0%;	Score 628.8;	DB 3;	Length 7560;
Best Local Similarity	77.8%;	Pred. No. 1e-99;		
Matches 759;	Conservative	0;	Mismatches 217;	Indels 0;
				Gaps 0;

[illegible]

QY 961 CCTCCGCGCTCTCTGA 976  
Db 2113 CTTCGGGGCGTCATGA 2128

RESULT 3  
US-09-598-421-20

; Sequence 20, Application US/09598421  
; Patent No. 6551825  
; GENERAL INFORMATION:  
; APPLICANT: Frazer Jr., Malcolm J.  
; APPLICANT: Shirk, Paul D.  
; APPLICANT: Elick, Teri A.  
; APPLICANT: Pereira, Ombethage  
; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic Transformation System  
; FILE REFERENCE: 0148.96  
; CURRENT APPLICATION NUMBER: US/09/598,421  
; CURRENT FILING DATE: 2000-06-19  
; PRIOR APPLICATION NUMBER: 60/016,234  
; PRIOR FILING DATE: 1996-04-19  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0 - Beta  
; SEQ ID NO 20  
; LENGTH: 7560  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: p3E1.2hs/opd  
US-09-598-421-20

Query Match 64.0%; Score 628.8; DB 4; Length 7560;

Best Local Similarity 77.8%; Pred. No. 1e-99; Matches 759; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 1 CGGCCGATCAACATCTCCGAGCGGGCTTCAACCTCAACCCAGACATCTGCGGCTC 60  
Db 1153 CGGCTCTATCAATCTCTGAAGCGGGTTTCACTGATCTCAAGACATCTGCGGCGAG 1212  
QY 61 CTCGCGCGGCTTCTCCGCGGCTTCCGCGGAGTTCTTCCGCTCCCGAGGCGCTTGGCGGA 120  
Db 1213 CTCGCGAGGATCTTGGCGGCTTGGCGAGATTCTTCCGTAACCGCAAGCTCTAGCGGA 1272  
QY 121 GAAGGCGGCGGCGGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
Db 1273 AAAAGCTGTGAAGAGATTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1332  
QY 181 GTTCACTTTCGACATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
Db 1333 GTTCACTTTCGACATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1392  
QY 241 CGTGCATCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
Db 1393 CGTTCATATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1452  
QY 301 CTCGCGTGAAGAGATCAACCAAGTTCTTCCGCGGAGATTCAGTACCGGATGAGAGACAC 360  
Db 1453 GAGTTAGAGAACTCAACAAGTTCTTCTCGGTGAGATTCAATATGAGCATGAAGACAC 1512  
QY 361 CGGCAATCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
Db 1513 CGGAAATTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1572  
QY 421 GCTGCTCTCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 480  
Db 1573 GTTAACTGTTAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1632  
QY 481 CACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540  
Db 1633 CACGCGAGAACTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1692  
QY 541 CTCCCGCTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600

Db 1693 GAGCCCTTCACGGGTTGTATGATGTCACAGCGATGATCTAGACGATTGAGCTATCTCAC 1752  
QY 601 CGCCCTTCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660  
Db 1753 CGCCCTTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1812  
QY 661 CTTGAGGACAAAGCGCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720  
Db 1813 TCTAAGAAATATAGGAGTGCATCAGCCCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1872  
QY 721 CTTCTCATCAAGGCGCTTCATGACCAAGGCTTACATGAAGAGATCTTGTGTCAACGA 780  
Db 1873 TCTCTTGAATCAAGGCGCTTCATGACCAAGGCTTACATGAAGAGATCTTGTGTCAACGA 1932  
QY 781 CTGAGCTTTCGCGCTTCTCTCTAGTGCACCAATCATGACGATGAGACCGGCGTGA 840  
Db 1933 CTGAGCTTTCGCGCTTTCGAGCTATGTACCAACATCATGACGATGAGATCGGCGTGA 1992  
QY 841 CCGGAGCGCATGAGCTTCATCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900  
Db 1993 CCGGAGCGGATGAGCTTCATTCATGAGATGATCCATTTCTTACGAGAGAGGCGCT 2052  
QY 901 GCGGAGAGAACCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960  
Db 2053 CCGACAGAAACGCTGGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2112  
QY 961 CCTCCGCGCTCTCTGA 976  
Db 2113 CTTCGGGGCGTCATGA 2128

RESULT 4  
5484728-1

; Patent No. 5484728  
; APPLICANT: SEERDAR, CUNEYI M.; MURDOCK, DOUGLAS  
; TITLE OF INVENTION: PARATHION HYDROLASE ANALOGS AND METHODS  
; FOR PRODUCTION AND PURIFICATION  
; NUMBER OF SEQUENCES: 6  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/333, 8892  
; FILING DATE: 01-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 898,973  
; FILING DATE: 25-JUN-1992  
; APPLICATION NUMBER: 312,503  
; FILING DATE: 17-FEB-1989  
; APPLICATION NUMBER: 237,255  
; FILING DATE: 26-AUG-1988  
; SEQ ID NO: 1  
; LENGTH: 1341  
5484728-1

Query Match 63.9%; Score 627.2; DB 6; Length 1341;

Best Local Similarity 77.7%; Pred. No. 1.8e-99; Matches 758; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

QY 1 CGGCCGATCAACATCTCCGAGCGGGCTTCAACCTCAACCCAGACATCTTGGGCGCTC 60  
Db 189 CGGCTCTATCAATCTCTGAAGCGGGTTTCACTGATCTCAAGACATCTTGGGCGGCGAG 248  
QY 61 CTCGCGCGGCTTCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120  
Db 249 CTCGCGAGGATCTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 308  
QY 121 GAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
Db 309 AAAAGCTGTGAAGAGATTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 368  
QY 181 GTTCACTTTCGACATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
Db 369 GTTCACTTTCGACATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 428

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QY 241 CTTGACATCTGTGCGCGCCACCGGCTCTGTGATCGACCCCGGCTCTCCATGCGCTCCG 300
D 429 CGTTATCTATCTGTGGCGCGACCGGCTTGTGTTCCACCCGCCACTTTCGATGCGATTGAG 488
QY 301 CTCGGTAGAGAGCTCACCCAGTTCTTCTCCGCGAGATCCAGTACCGGATCGAGAGAC 360
D 489 GAGGTAGAGAACTCACAGTTCTTCTGCTGAGATTCATATGGATCGAAGACAC 548
QY 361 CGGCATCCGCGCGGATCATCAAGGTGACCAACCGGCAAGGCAAGCCGCTTCAGAGA 420
D 549 CGGAATTAGGGCGGCAATTATCAAGTGCACACCAAGGCAAGGCAAGCCGCTTCAGAGA 608
QY 421 GCTGTGCTCAAGGCGCGCGCGCTCTCCCTCCGACCGGCGTGGGATGACCA 480
D 609 GTTAGTGTAAAGGCGCGCGCGCGGCAAGTTCGACACCGGTGTTCGGTAACTCA 668
QY 481 CACGCGCGCTCCGACGCGGAGACGCGGACAGCGGCGGCACTTCGATCCGAGGCGCT 540
D 669 CACGCGACAGTCAAGCGCGAGTGTAGAGACAGCGGCGGCACTTTCGATCCGAGGCGCT 728
QY 541 CTCGCGCTCCGCGGTGTGATCGGCACTCGGACGACGACGACGACGCTCTCCATCTGAC 600
D 729 GAGCGCCCTCAGGGGTTTGTATGTCACAGGATGATCTGACGATTTGAGCTATCTCAC 788
QY 601 CGCCTTCGCGCGCGCGGCTACCTGATCGGCTCGACCATCCGCACTCCGCACTCGG 660
D 789 CGCCTTCGCTCGCGCGGATACCTCATCGGTCTAGACCAATCCGCAAGTGCATTGG 848
QY 661 CCTGAGGAGCAACGCTCCGCGTCCGCTCCGCGGATCCGCTCGGAGACCGGCGC 720
D 849 TCTAGAGATTAATGAGATGATCAGCCCTCTGCGGCACTCGTTGCGGAAACGCGGC 908
QY 721 CCTCTCATCAAGGCGCTCATCGACCAAGGCTACATGAAAGATCTCTGTATCCAGCA 780
D 909 TCTCTGATCAAGGCGCTCATCGACCAAGGCTACATGAAAGATCTCTGTATCCAGCA 968
QY 781 CTGCTCTTGGGCTTCTCTCTAGTGAACCAATCATGACGTGATGACCGGCTGAA 840
D 969 CTGCTGTTCGGGTTTTCGAGTATGTCAACCAATCATGACGTGATGATCGGCTGAA 1028
QY 841 CCGGAGCGGATGCGCTTCATCCGCGCTCCGCGTATCCGCTCTCCGCGAAGAGGCGT 900
D 1029 CCGGAGCGGATGCGCTTCATCCGCGCTTCGAGATGATCCATTCCTACAGAGAGAGGCGT 1088
QY 901 GCGGAGAGAGACCTTCGCGGATCAACCGTGAACCAACCGGCGGCTTCCTCTCCGAC 960
D 1089 CCGGAGAGAGAGCGCTGCGAGGATCATGTGACTTAACCGGCGGCTTCCTGTCACGAC 1148
QY 961 CCGCGGCGCTCTCTGA 976
D 1149 CTTGCGGCGCTCATGA 1164
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RESULT 5
5484728-1
; Patent No. 5484728
; APPLICANT: SEERDAR, CUNEYT M.; MURDOCK, DOUGLAS
; TITLE OF INVENTION: PARATHION HYDROLASE ANALOGS AND METHODS
; FOR PRODUCTION AND PURIFICATION
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333, 8892
; FILING DATE: 01-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 898, 973
; FILING DATE: 25-JUN-1992
; APPLICATION NUMBER: 312,503
; FILING DATE: 17-FEB-1989
; APPLICATION NUMBER: 237, 255
; FILING DATE: 26-AUG-1988
; SEQ ID NO: 1:
; LENGTH: 1341
5484728-1
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Query Match 63.9%; Score 627.2; DB 6; Length 1341;
Best Local Similarity 77.7%; Pred. No. 1.8e-99;
Matches 758; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

QY 1 CCGCCCATCAACATCTCCGAGCGGCTTCACTTCACTCAAGGACATCTGGGCTC 60
D 189 CGGTCTATCAACATCTCTGAAGCGGCTTCACTGCTACAGCAATCTGGGCGAG 248
QY 61 CTCGCGCGCTTCTCCGCGCTGAGGATTTCTTGGCTCCGCAAGGCGCTCGCGGA 120
D 249 CTCGCGAGGATTTCTGCGCTTGTGGCAGAGTTCTTGGATGCGGCAAGCTCTTAGCGGA 308
QY 121 GAAGCGCTGCGCGGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
D 309 AAGGCTGTGAGAGGATTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 368
QY 181 GTTCACTTGCACATCGGCGCGGACGTCTCTCTGCGGAGGTGTCCGCGCGCGCGCG 240
D 369 GTGACTTTGATATCGGTTCGCGAGTCAAGTTTATGGCCGAGGTTTCGCGGCGTCCGA 428
QY 241 CTTGACATCTGTGCGCGCAACCGGCTCTGATTCGACCGGCGCTCTCATGCGCTCCG 300
D 429 CGTTATATCTGTGCGCGGACCGGCTTGTGATGACCGGCACTTTCGATGCGATTGAG 488
QY 301 CTCGGTAGAGAGCTCAACCAAGTTCTTCTTCGCGGAGATTCAGTACGGGATCGAGAGAC 360
D 489 GAGGTAGAGAGACTCACACAGTTCTTCTCTGAGATTCATATGAGCATCGAAGACAC 548
QY 361 CCGGATCCGCGCGGATCATCAAGGTGCGGACCAACCGGCAAGGCAAGCCGCTTCAGAGA 420
D 549 CGGAATTAGGGCGGCAATTATCAAGGTGCGGACCAACAGGCAAGGCAAGCCCTTTCAGAGA 608
QY 421 GCTGTGCTCAAGGCGCGCGCGCTCTCCGCGGCAACCGGCTGCGGATGACCA 480
D 609 GTTAGTGTAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 668
QY 481 CACGCGCGCTTCCGAGCGGACGCGGAGACGAGGCGGCGGCACTTCGAGTCCAGAGGCT 540
D 669 CACGCGAGCAAGTCAAGCGGATGATGAGGACGAGGCGGCGGCACTTTCGAGTCCGAGGCT 728
QY 541 CTCGCGCGCGCGGCTGTGATCGGCACTCCGCGGCAACCGGCAACCGGCTCTCTCTAC 600
D 729 GAGCGCCCTCAGGGGTTTGTATGTCACAGGATGATTCGACATTTGAGCTTCTCAC 788
QY 721 CCTCTCATCAAGGCGCTCATCGACCAAGGCTACATGAAAGATCTCTGTATCCAGCA 780
D 909 TCTCTGATCAAGGCGCTCATCGACCAAGGCTACATGAAAGATCTCTGTATCCAGCA 968
QY 781 CTGCTCTTGGGCTTCTCTCTAGTGAACCAATCATGACGTGATGACCGGCTGAA 840
D 969 CTGCTGTTCGGGTTTTCGAGTATGTCAACCAATCATGACGTGATGATCGGCTGAA 1028
QY 841 CCGGAGCGGATGCGCTTCATCCGCGCTTCGCGTATCCGCTCTCCGCGAAGAGGCGT 900
D 1029 CCGGAGCGGATGCGCTTCATCCGCGCTTCGAGATGATCCATTCCTACAGAGAGAGGCGT 1088
QY 901 GCGGAGAGAGACCTTCGCGGATCAACCGTGAACCAACCGGCGGCTTCCTCTCCGAC 960
D 1089 CCGGAGAGAGAGCGCTGCGAGGATCATGTGACTTAACCGGCGGCTTCCTGTCACGAC 1148
QY 961 CCGCGGCGCTCTCTGA 976
D 1149 CTTGCGGCGCTCATGA 1164
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RESULT 6  
US-09-603-450-3  
; Sequence 3, Application US/09603450  
; Patent No. 6469145  
; GENERAL INFORMATION:  
; APPLICANT: Raetog1, Vapin K  
; APPLICANT: Cheng, Tu-c  
; APPLICANT: Defrank, Joseph J  
; TITLE OF INVENTION: One-Step Purification Process for Organophosphorus  
; TITLE OF INVENTION: Hydrolyase Enzyme  
; FILE REFERENCE: DAM-508-99  
; CURRENT APPLICATION NUMBER: US/09/603,450  
; CURRENT FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 1693  
; TYPE: DNA  
; ORGANISM: Flavobacterium sp  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (506)..(1516)  
; OTHER INFORMATION: Expresses organophosphorus hydrolase  
; NAME/KEY: sig\_peptide  
; LOCATION: (419)..(505)  
; OTHER INFORMATION: Removal of signal peptide allows organophosphorus  
; OTHER INFORMATION: hydrolase to be expressed in soluble form  
US-09-603-450-3

Query Match 63.9%; Score 627.2; DB 3; Length 1693;  
Best Local Similarity 77.7%; Pred. No. 1.8e-99;  
Matches 758; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

QY 1 CGGCCGATACCATCTCCGAGCGCGCTTCACTCCACCCAGACACATCTCGCGCTC 60  
DB 541 CGGCTCTATCAAACTCTGAAGCGGGTTTCACTGACTCAAGACATCTCGCGCGAG 600  
QY 61 CTCGCGCGCTTCTCCGCGCGCTGCGCGAGTTCTTCGCGCTCCGGAAGCCCTCGCGCA 120  
DB 601 CTCGCGAGATTCTTGGCGCTTGGCGAGATTCTTCGCGAGCGGAAAGCTCTTACGCGA 660  
QY 121 GAAGCGCGTGCAGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
DB 661 AAAGCGTGTGAAGAGATTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720  
QY 181 GTCCACTTTCGACATCG 240  
DB 721 GTTCGACTTTCGATTCG 780  
QY 241 CGTGCACATCGTGGCG 300  
DB 781 CGTTATATCGTGGCG 840  
QY 301 CTCGCGAGAGCTCAACCAAGTTCTTCTCCGCGAGATCCAGTACGCGATCGAGGACAC 360  
DB 841 GAGGTGAGAGAACTCAACAAGTTCTTCTCGGTGAGATTCAATAGGATCGAAGACAC 900  
QY 361 CGGCAATCG 420  
DB 901 CGGAATTAGGGCGGGCATTTATCAAGGTCCGACCAAGGCAAGGCAAGCCCTTTACAGA 960  
QY 421 GCTCGTGTCAAGCG 480  
DB 961 GTTAGGTAAAGCG 1020  
QY 481 CAACGCGCGCTCCAGCG 540  
DB 1021 CACGCGAGAAAGTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080  
QY 541 CTCGCCGCTCGCGGTGTGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600  
DB 1081 GAGCCCTCAGCGGTTTGTATGGTCAAGCGCGATGATGAGATTTGAGCTATCTCAC 1140

QY 601 CGCCCTCCGCGCGCGCTACTCATCGAGCTCGACCAATCCGCACTCCGCCATCG 660  
DB 1141 CGCCCTCCGCGCGCGGATTAAGTCTATCGGTCTAAGCAATCCGCAAGTGGCATTTGG 1200  
QY 661 CTTGAGAGAAAGCTTCCGCGCTCCGCGCTTCTCGGCAATCCGCTCTCGGACACCGCGC 720  
DB 1201 TCTAGAAATATATGCGATGATCAAGCCCTCTCGGCAATCCGCTCTCGGCAAGCGGCG 1260  
QY 721 CTTCTCATCAAGCGCTCATGACAGGCGCTCAATGAAGAGATCTGTGTCAAGCA 780  
DB 1261 TCTTGTATCAAGCGCTCATGACAGGCGCTCAATGAAGAGATCTGTGTCAAGCA 1320  
QY 781 CTGCTCTTGGCTTCTCTCTTACGTAACCAATCATGAGATGAGACCGCGTGA 840  
DB 1321 CTGCTGTTCGCGTTTTCAGAGTATGTACCAACATCATGAGATGAGATCGGCTGA 1380  
QY 841 CCGGACGCGATGCGCTTTCATCGCGCTCCGCGGTATCCCGTCTCTCCGAGAAAGGCGT 900  
DB 1381 CCGGACGCGATGCGCTTTCATCGCGCTCCGCGGTATCCCGTCTCTCCGAGAAAGGCGT 1440  
QY 901 GCGGAGAGAACCTTCGCGCGATCAAGCGTAACCGCGCGCTTCTCCCGGAC 960  
DB 1441 CCGACAGAAAGCTGCGAGCATCATGATGATTAACCGCGCGCTTCTCTTCAACGAC 1500  
QY 961 CTTCCGCGCTCTCTGA 976  
DB 1501 CTTGCGGCGCTCATGA 1516

RESULT 7  
US-08-844-274-14/c  
; Sequence 14, Application US/08844274B  
; Patent No. 6218185  
; GENERAL INFORMATION:  
; APPLICANT: Fraser Jr., Malcolm J.  
; APPLICANT: Shirk, Paul D.  
; APPLICANT: Ellick, Teri A.  
; APPLICANT: Perera, Omachage  
; TITLE OF INVENTION: Piggybac Transposon-Based Genetic Transformation System  
; TITLE OF INVENTION: for Insects  
; FILE REFERENCE: 0148.96  
; CURRENT APPLICATION NUMBER: US/08/844,274B  
; CURRENT FILING DATE: 1997-04-18  
; EARLIER APPLICATION NUMBER: 60/016,234  
; EARLIER FILING DATE: 1996-04-19  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0 - beta  
; SEQ ID NO 14  
; LENGTH: 6723  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: piggyBac/opd  
US-08-844-274-14

Query Match 63.9%; Score 627.2; DB 3; Length 6723;  
Best Local Similarity 77.7%; Pred. No. 1.9e-99;  
Matches 758; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

QY 1 CGGCCGATACCATCTCCGAGCGCGCTTCACTCCACCCAGACACATCTCGCGCTC 60  
DB 4194 CGGCTCTATCAAACTCTGAAGCGGGTTTCACTGACTCAAGACATCTCGCGCGAG 4135  
QY 61 CTCGCGCGCTTCTCCGCGCGCTGCGCGAGTTCTTCGCGCTCCGGAAGCCCTCGCGCA 120  
DB 4134 CTCGCGAGATTCTTGGCGGCTTGGCGAGAGTTCTTCGCTACCGGAAAGCTTACGCGA 4075  
QY 121 GAAGCGCGTGCAGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
DB 4074 AAAGCGTGTGAAGAGATTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4015  
QY 181 GTCCACTTTCGACATCG 240

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Db 4014 GTGACCTTTCATATCGTGGAGCTCACTTATTTGGCGAGGTTTGGCGGAGCTGACCA 3955
Qy 241 CGTGACATTCGTGGCGGACCGGCTCTGTTTCGACCCGCGCTCTCCATGCGCTCCG 300
Db 3954 CGTTATATTCGTGGGCGGACCGGCTGTGGTTTCGACCCGCACTTTCATTCGATGAG 3895
Qy 301 CTCCTGAGAGCTCAACCACTTCTCTCCGAGATTCAGTACGGATCGAGACAC 360
Db 3894 GAGTGTAGGAGAACTACACAGTTCTCTCGGTGAGATTCAATATGCGATCGAAGACAC 3835
Qy 361 CGGCATCCGCGCGGATATCAAGTGGCCACACCGGCAAGGCCACCCCTTCCAGA 420
Db 3834 CGGAATTAGGCGGCGCATTTATCAAGGTGCGACACAGGCAAGGAGACCCCTTTCAGA 3775
Qy 421 GCTCGTCAAGGCGCGCGCGGCTCTCTCCGACCGGCGGTGGACCAACCA 480
Db 3774 GTTACTGTTAAAGGGGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3715
Qy 481 CACGCGCGCTCTCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
Db 3714 CACGCGAGAGTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3655
Qy 541 CTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
Db 3654 GAGCCCTTCACGGGTTTGTATGTGTCACGCGATGATGACGATTGAGCTATCTCAC 3595
Qy 601 CGCCCTCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Db 3594 CGCCCTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3535
Qy 661 CCTCGAGACACCGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Db 3534 TCTAAGATATATGAGATGATCAAGCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGG 3475
Qy 721 CCTCTCATCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
Db 3474 TCTCTTATCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3415
Qy 781 CTGGCTCTTCGCGCTTCTCTCTCAAGTACCAATCATGAGCTGATGACCGGCGTAA 840
Db 3414 CTGGCTCTTCGCGGCTTCTCTCTCAAGTACCAATCATGAGCTGATGAGCTGATGAG 3355
Qy 841 CCGGAGCGGCGGCTTCTCTCTCAAGTACCAATCATGAGCTGATGAGCTGATGAGCTG 900
Db 3354 CCGGAGCGGCGGCTTCTCTCTCAAGTACCAATCATGAGCTGATGAGCTGATGAGCTG 3295
Qy 901 GCGGAGGAGACCGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960
Db 3294 CCGGAGGAGACCGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3235
Qy 961 CCTCGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 976
Db 3234 CTTGGCGGCGGCTCATGA 3219

RESULT 8
US-09-598-421-14/c
; Sequence 14, Application US/09598421
; Patent No. 6551825
; GENERAL INFORMATION:
; APPLICANT: Fraser Jr., Malcom J.
; APPLICANT: Shirk, Paul D.
; APPLICANT: Elick, Teri A.
; APPLICANT: Pereira, Omalahage
; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic Transformation System
; TITLE OF INVENTION: for Insects
; FILE REFERENCE: 0148.96
; CURRENT APPLICATION NUMBER: US/09/598.421
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 60/016,234
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 22
```

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; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 14
; LENGTH: 6723
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: piggyBac/opd
US-09-598-421-14

Query Match      63.9%; Score 627.2; DB 4; Length 6723;
Beet Local Similarity 77.7%; Pred. No. 1.9e-99;
Matches 758; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

Qy 1 CGGCGGATCAACATCTTCGAGCGCGGCTTCAACCTCAACCAAGCAATCTGCGGCTC 60
Db 4194 CGGTCTTATCAACATCTTCGAGCGGCGGCTTCAACCTCAACCAAGCAATCTGCGGCGG 4135
Qy 61 CTCGCGCGGCTTCTCTCGCGGCTGCGGAGTTCTTGGCTTCCGCAAGGCGCTGCGG 120
Db 4134 CTCGCGAGGATTTCTGCGGCTTGGCGGAGTTCTTGGTGGCGGCAAGGCTTCAAGCGG 4075
Qy 121 GAAGCGGTGCGGCGGCTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
Db 4074 AAGGCTGTGAGAGGATTTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4015
Qy 181 GTCACTTTGCAATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 4014 GTGACCTTTCATATCGGTCGCGAGCTGATTTAGCGAGGTTTCGCGGCGGCGGCGG 3955
Qy 241 CGTGACATTCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 3954 CGTTATATTCGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3895
Qy 301 CTCGTTGAGAGCTCAACCACTTCTCTCTCGGAGATTCAGTACGGATCGAGACAC 360
Db 3894 GAGTGTAGGAGAACTACACAGTTCTCTCTCGGAGATTCAGTACGGATCGAGACAC 3835
Qy 361 CGGCATCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Db 3834 CGGAATTAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3775
Qy 421 GCTCGTCTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Db 3774 GTTGTGTTTAAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3715
Qy 481 CACGCGCGCTCTCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
Db 3714 CACGCGAGAGTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3655
Qy 541 CTCGCGCGTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
Db 3654 GAGCCCTTCACGGGTTTGTATGTGTCACGCGATGATGACGATTGAGCTATCTCAC 3595
Qy 601 CGCCCTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Db 3594 CGCCCTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3535
Qy 661 CCTCGAGACACCGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Db 3534 TCTAAGATATATGAGATGATCAAGCTCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGG 3475
Qy 721 CCTCTCATCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
Db 3474 TCTCTTATCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3415
Qy 781 CTGGCTCTTCGCGCTTCTCTCTCAAGTACCAATCATGAGCTGATGAGCTGATGAGCTG 840
Db 3414 CTGGCTCTTCGCGGCTTCTCTCTCAAGTACCAATCATGAGCTGATGAGCTGATGAGCTG 3355
Qy 841 CCGGAGCGGCGGCTTCTCTCTCAAGTACCAATCATGAGCTGATGAGCTGATGAGCTG 900
Db 3354 CCGGAGCGGAGTGGCTTCTCTCTCAAGTACCAATCATGAGCTGATGAGCTGATGAGCTG 3295
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Qy 901 GCCGAGAGACCTTCGCGGATCAACCGACCCGCTTCTCTCCCGAC 960  
Db 3294 CCCACAGAAACGCTGGCAGGATCATCTGTACTAACCCGGGGCGGTTCTTGACGAC 3235  
Qy 961 CCTCGCGCCTCTCTGA 976  
Db 3234 CTGGCGGCGCTCATGA 3219

## RESULT 9

US-08-844-274-13  
; Sequence 13, Application US/08844274B  
; Patent No. 6218185  
; GENERAL INFORMATION:  
; APPLICANT: Fraser Jr., Malcom J.  
; APPLICANT: Shirk, Paul D.  
; APPLICANT: Ellick, Teri A.  
; APPLICANT: Perera, Omachthage  
; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic Transformation System  
; FILE REFERENCE: 0148.96  
; CURRENT APPLICATION NUMBER: US/08/844,274B  
; CURRENT FILING DATE: 1997-04-18  
; EARLIER APPLICATION NUMBER: 60/016,234  
; EARLIER FILING DATE: 1996-04-19  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0 - beta  
; SEQ ID NO 13  
; LENGTH: 6723  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Clone p3el.2H/S  
US-08-844-274-13

Query Match 63.5%; Score 624; DB 3; Length 6723;  
Best Local Similarity 77.5%; Pred. No. 6.7e-99;  
Matches 756; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

Qy 1 CGGCGCATCAACCATCTCCGAGCGCGCTTCACTCCACCCAGACATCTGGGCTC 60  
Db 2530 CGGTCTATCAACATCTCTGAAGCGGGTTTCACTCAAGACATCTGGCGAG 2589  
Qy 61 CTCGCGCGCTTCTCCGCGCTTCGCGGAGTTCTTGGCTCCCGCAAGGCCCTCGCGCA 120  
Db 2550 CTCGCGAGATTTCTGCTGCTTGGCGAGAGTTCTTGGTAGCCGAAAGCTTGAAGCGGA 2649  
Qy 121 GAAGGCGTGGCGGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTGCACCATCTGAGAGCT 180  
Db 2650 AAAGGCTGTGAAGAGATTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTGTGATGT 2709  
Qy 181 GTCCACCTTTCACATCG 240  
Db 2710 GTCCACCTTTCACATCG 2769  
Qy 241 CGTGACATCTGGCG 300  
Db 2770 CGTTATATCTGGCG 2829  
Qy 301 CTCGCTGAGAGAGCTCAACCACTTCTTCTCCGAGATCGATCGAGAGAGAG 360  
Db 2830 GAGGTAGAGAGAGCTCAACCACTTCTTCTCCGAGATCGATCGAGAGAGAG 2889  
Qy 361 CGGATTCG 420  
Db 2890 CGGATTCG 2949  
Qy 421 GCTCTGTCTCAAGCG 480  
Db 2950 GTTATGTCTTAAAGCG 3009  
Qy 481 CACCGCGCTTCCAGCG 540  
Db 481 CACCGCGCTTCCAGCG 540

Db 3010 CACGAGCAAGTACGCGCGATGAGTGAAGACAGAGCGCCATTTTGAATCCGAGGCTT 3069  
Qy 541 CTCGCCGTCG 600  
Db 3070 GAGCCCTTACAGCGGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3129  
Qy 601 CGCCCTCG 660  
Db 3130 CGCCCTCG 3189  
Qy 661 CTGAGAGACACCGCTTCG 720  
Db 3190 TCTAGAGATATATGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3249  
Qy 721 CCTCTCATCAAGGCG 780  
Db 3250 TCTCTTATCAAGGCG 3309  
Qy 781 CTGCTCTTCTGCGCTTCT 840  
Db 3310 CTGCTCTTCTGCGCTTCT 3369  
Qy 841 CCCGAGCGCATGCGCTTCT 900  
Db 3370 CCCGAGCGCATGCGCTTCT 3429  
Qy 901 GCCGAGGAGACCGCTTCG 960  
Db 3430 CCCAGAGAAACGCTTGGCAGGATCATCTGTACTTACCTAACCCGCGCGGTTCTTGACCGAC 3489  
Qy 961 CCTCGCGCCTCTCTGA 976  
Db 3490 CTGGCGGCGCTCATGA 3505

## RESULT 10

US-09-598-421-13  
; Sequence 13, Application US/09598421  
; Patent No. 6551825  
; GENERAL INFORMATION:  
; APPLICANT: Fraser Jr., Malcom J.  
; APPLICANT: Shirk, Paul D.  
; APPLICANT: Ellick, Teri A.  
; APPLICANT: Perera, Omachthage  
; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic Transformation System  
; FILE REFERENCE: 0148.96  
; CURRENT APPLICATION NUMBER: US/09/598,421  
; CURRENT FILING DATE: 2000-06-19  
; PRIOR APPLICATION NUMBER: 60/016,234  
; PRIOR FILING DATE: 1996-04-19  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0 - beta  
; SEQ ID NO 13  
; LENGTH: 6723  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Clone p3el.2H/S  
US-09-598-421-13

Query Match 63.5%; Score 624; DB 4; Length 6723;  
Best Local Similarity 77.5%; Pred. No. 6.7e-99;  
Matches 756; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

Qy 1 CGGCGCATCAACCATCTCCGAGCGCGCTTCACTCCACCCAGACATCTGGGCTC 60  
Db 2530 CGGTCTATCAACATCTCTGAAGCGGGTTTCACTCAAGACATCTGGCGAG 2589  
Qy 61 CTCGCGCGCTTCTCCGCGCTTCGCGGAGTTCTTGGCTCCCGCAAGGCCCTCGCGCA 120  
Db 2590 CTCGCGAGATTTCTGCTGCTTGGCGAGAGTTCTTGGTAGCCGAAAGCTTGAAGCGGA 2649

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QY 121 GAAGCCGTCGCGGCTCCGCGCGCCGCGCGCGCGCTGCGCACATCGTAGAGT 180
D 2550 AAAGCTGTGAGAGATTGCGCGCGCCAGAGCGGCTGGCGGCAATGTGTGATGT 2709
QY 181 GTCCACCTTGCACATCGGCGCGCGAGTGTCCCTCTCGCGGAGGTGTCCCGCGCGGA 240
D 2710 GTCCACTTTCATATCGGTGCGGAGCTGATTTATTTGCGCGAGGTTTGGCGGCGCGGA 2769
QY 241 CGTGACATCGTGGCGCGCGCGCGCTGTGTTTCAGCCGCGCTCTCATGCGCTCG 300
D 2770 CGTTTATTCGTGGCGCGGAGCGCGCTGTGTGTGACCGCGCATTTGATGCGATTAG 2829
QY 301 CTCGTGAGAGAGCTCACCCAGTTCTTCTCGCGAGATTCAGTACGCGATCGAGACAC 360
D 2830 GAGTGTAGAGAACTCACACAGTTCTTCTCGGTGAGATTCAATATGCGATCGAAGACAC 2889
QY 361 CGGATCGCGCGCGCGCATCATCAAGGTGCGCACCGCGCAAGGCGCACCGCTTCCAGA 420
D 2890 CGAATTAGGCGCGCGCATTTATCAAGTGTGCGACACAGCGCAAGGCGCACCGCTTCCAGA 2949
QY 421 GCTGTGCTCAAGCGCGCGCGCGCGCTCTCCCTCGCGCACCGCGCGGTGACCGCA 480
D 2950 GTTAGTGTAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3009
QY 481 CACGCGCGCTTCCAGCGCGCGAGCGAGACAGCGCGCGCGCGCGCGCGCGCGCGCT 540
D 3010 CACGCGAGCAAGTCAAGCGCGAGTGTGAGACAGCGCGCGCGCGCGCGCGCGCGCGCT 3069
QY 541 CTCGCGCGCGCGCGGTGCGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
D 3070 GAGCGCGCGCGCGCGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 3129
QY 601 CGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
D 3130 CGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3189
QY 661 CCTGAGAGACAAGCTTCGCGCGTCCGCTCTCGCGAGATCGCGCTTCTGAGACCGCG 720
D 3190 TCTGAAATATATGAGATGATCAAGCGCGCTCTCGCGCGCGCGCGCGCGCGCGCG 3249
QY 721 CCTCTCATCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
D 3250 TCTCTTATCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3309
QY 781 CTGCTCTTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
D 3310 CTGCTGTTGCGGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3369
QY 841 CCGGAGCGCGATGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
D 3370 CCGGAGCGCGATGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3429
QY 901 GCGGAGGAGAGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
D 3430 CCGGAGGAGAGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3489
QY 961 CCTCGCGCGCTCTCTGA 976
D 3490 CTTGCGGCGCTCATGA 3505

RESULT 11
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
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; CURRENT APPLICATION NUMBER: US/09/103, 840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 16.9%; Score 166.4; DB 3; Length 4403765;
Best Local Similarity 55.5%; Pred. No. 4e-20;
Matches 382; Conservative 0; Mismatches 276; Indels 30; Gaps 2;

QY 1 CGGCGCGATCACATCTTCGAGCGCGCGCTTACCTTACCCGAGACATCTGCGCTC 60
D 276050 CGGACCCATCGACACCGCTGATCTCGGCGTCAAGCTGATGACGACGCTTTCATCAT 275991
QY 61 CTCGCGCGCTTCTCTCGCGCGCTGCGCGAGTTCTTGGCTTCCGCAAGCGCTTCCGGA 120
D 275990 GACCAAGATGATGCGCGAGAACTACCGGAGCGCTTGGGCGATCAGAGCAAGCGGTTGC 275931
QY 121 GAAGCGCGTGGCGGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
D 275930 CGGCGCGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 275871
QY 181 GTCCACTTGCACATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
D 275870 CACGATGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 275811
QY 241 CGTGCACATCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
D 275810 GCTAACAATCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 275751
QY 301 CTCGCT-----GAGGAGCTCACCCAGTTCTTCTCTCG 333
D 275750 CTACTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 275691
QY 334 CGAATTCAGTACGCGCGATCGAGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 393
D 275690 CGAATTCAGTACGCGCGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 275631
QY 394 CACCGGAGAGCG---CACCGCGCTTCCAGAGCTGTGCTCAAGGCGCGCGCGCGCGCTC 450
D 275630 CGAGGAAACCGCGCGCTCACCGCTGTGTGAGCGGCGGTGCGCGCGCGCGCGCG 275571
QY 451 CCTCGCGACCGCGCGTGCCTGAGCACCAACCGCGCGCTCCGAGCGCGAGCGCA 510
D 275570 CAAAGCAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTGA 275511
QY 511 GCAGCGCGCGATCTTTCAGATCGAGGCGCTTCCCGCTCGCGGTGTGATCGGCGCACT 570
D 275510 CCAAGCAAGCATCTTTCGCGCGAGGAGGCGGTGAGCTGAGCGGCGGTGTTATCGGA 275451
QY 571 CGAGGACACCGACGACCTTCTCTTACCTTACCGCGCGCTCGCGCGCGCGCGCGCTT 630
D 275450 CGGCGACGACCGACGCGCGCTTCTTACCTTACCTTACCTTACCTTACCTTACCT 275391
QY 631 CCTGACACATCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 658
D 275390 GATGACCGGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 275363

RESULT 12
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
```

APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
TITLE OF INVENTION: TUBERCULOSIS  
FILE REFERENCE: 2436-2007.00  
CURRENT APPLICATION NUMBER: US/09/103,840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 1  
LENGTH: 4411529  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 16.9%; Score 166.4; DB 3; Length 4411529;  
Best Local Similarity 55.5%; Pred. No. 4e-20;  
Matches 382; Conservative 0; Mismatches 276; Indels 30; Gaps 2;

QY 1 CGGCGCATACATCTCCGAGCCGGCTTCACTCCCTCAACCCAGACATCTCGGCTC 60  
DB 275938 CGGACCCATCGACACCGCTGATCTCGCGTCAAGTATGACAGACATCTTCATCAT 275879  
QY 61 CTCGCGCGCTTCTCCGCGCTGCGCGAGTTCTTCGCGCTCCGCGAGGCCCTCGCGCA 120  
DB 275878 GACCCCGAGATGCGCGAGAACTACCCGAGCTCGGCGAGAGAGACAGCGGCTGCG 275819  
QY 121 GAAGCGCGTGGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
DB 275818 CGGCGCGATCGCGCGCTAGAGAACTCAAGCGCGCGCGCGCGCGCGCGCGCGCG 275759  
QY 181 GTCCACCTTCCAGATCG 240  
DB 275758 CAGCGTATCG 275699  
QY 241 CGTGCATCGTGGCG 300  
DB 275698 GCTGAACATCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 275639  
QY 301 CTCGCT-----GAGAGACTCACCGATTCTTCCTCG 333  
DB 275638 CTACCTCGGCG 275579  
QY 334 CGAGATCCAGTACCG 393  
DB 275578 CGACATCGAGCG 275519  
QY 394 CACCGCGAGGCG---CACCGCGTTCAGGAGCTCGTCAAGCGCGCGCGCGCGCGCGCG 450  
DB 275518 CGAGCAACCG 275459  
QY 451 CTTGCGCAACCG 510  
DB 275458 CAAGCGACCG 275399  
QY 511 GCAAGCG 570  
DB 275398 CGAGACCG 275339  
QY 571 CGACGACCG 630  
DB 275338 CGGCGACGACCG 275279  
QY 631 CTTGACCAATCCCGCATCCGCGCATC 658  
DB 275278 GATGACCGGTTCCGCGTGCAGTATC 275251

RESULT 13  
US-09-249-585A-4  
; Sequence 4, Application US/09249585A

Patent No. 6417002  
GENERAL INFORMATION:  
APPLICANT: Horlick, Robert  
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES  
FILE REFERENCE: 0867/0905  
CURRENT APPLICATION NUMBER: US/09/249,585A  
CURRENT FILING DATE: 1999-02-11  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 4  
LENGTH: 1926  
TYPE: DNA  
ORGANISM: Epstein Barr Virus  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(1926)  
OTHER INFORMATION: template strand of EBNA-1 DNA  
US-09-249-585A-4

Query Match 14.0%; Score 137; DB 3; Length 1926;  
Best Local Similarity 48.8%; Pred. No. 3.4e-15;  
Matches 464; Conservative 0; Mismatches 475; Indels 12; Gaps 3;

QY 32 ACCCTCACCCAGACACATCTCGGCTCTCCGCGGCTTCTCCGCGCTGCGCGAG 91  
DB 117 ACCTGCTCTGCGCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 176  
QY 92 TTTCTTGGCTCCCGAGAGCCCTCGCGAGAAAGCGGCGGCTCCGCGCGCGCG 151  
DB 177 GAGTCTAGTCCCGGCTTCTGATCTTACACAGGCTCTGGGCTTTTGGAGTTCAAC 236  
QY 152 GCGCGCGGCGCGCGACCATGTGAGCGTGCAC--CTTGCATTCGCGCGCGAGTGT 209  
DB 237 GTAACGAGATTCTCTGAGTGCACCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 296  
QY 210 CCTCTCTGCGCGAGTGTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 269  
DB 297 TGTCTCTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 356  
QY 270 GGTGTGACCGCGCGCTCTGACGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 329  
DB 357 TCCCGGCTCTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 416  
QY 330 TCCGCGATTCAGTACGCGCATGAGGACACCGCGCATCGCGCGCGCGCATCAAGTGT 389  
DB 417 TCTCTCCGCTCTGCT 476  
QY 390 CCACGACCGCGAGGCGCACCCCGTTCCAGAGCTGTGTCAAGCGCGCGCGCGCGCGCT 449  
DB 477 TCTCTCCGCT 536  
QY 450 CCTTGCACCGCGGCTGCGGAGTACACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 509  
DB 537 TCCCGGCTCTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 566  
QY 510 AGCAGCGCGCATCTTGCAGTGCAGGCGCTTCCCGGCGCGCGCGCGCGCGCGCGCAT 569  
DB 597 TCTCTCCGCTCTGCT 656  
QY 570 CGAGACGACGACGATCTTCTTACCTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCAT 629  
DB 657 TGTCT 713  
QY 630 GCTTGCACGACATCCCGCATCTCGCGCATGTGAGGAGCAAGCGCTCTCGCGCGCG 689  
DB 714 TCCCGGCT 773  
QY 690 TCTTGGAGATCGCTCTGCGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 749  
DB 774 TCTCTCCGCTCTGCT 833  
QY 750 GCTACATGAGGAGATCTGCTGTCAGAGCATGTGAGCTTCTGCGCTTCTCTTACGTA 809



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;
;   REGISTRATION NUMBER: 25,146
;   REFERENCE/DOCKET NUMBER: 03806.0054-00000
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 408-4000
;   TELEFAX: (202) 408-4400
;   INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1208 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;   ORGANISM: S.priestinaespiralis
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..1208
;   US-08-403-852D-4

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Query Match      11.3%; Score 110.8; DB 2; Length 1208;
Best Local Similarity 47.1%; Pred.No.1.1e-10;
Matches 469; Conservative 0; Mismatches 497; Indels 30; Gaps 3;

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QY 13 CATCTCCGAGCGCGGCTTCAACCTTCAACCCAGAGCAATCTGGGCTCTCCGCGGCTT 72
DB 18 CACCTTCGAGTCCGTGACCGAGGCGCCACCCCAAGATCGCCGACCAATCAGTACAC 77
QY 73 CCTCCGCGCTTGAGCGGAGTTCTTCCGCTCCCGCAAGGCTTCCGCGAGAGCGCGTGC 132
DB 78 CGTCTCGACGCGCTGTGTCGCGAGAGACCCGCGCTTCAACGCTCGCGGTGAGACCTGAT 137
QY 133 CGGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 192
DB 138 CACCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 197
QY 193 CATCGGCGCGCGAGGTCCTTCCGCGAGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 252
DB 198 CCAACTGTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 257
QY 253 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 312
DB 258 CGGCGCGCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 317
QY 313 GCTTACCGAGTTCT-----TCTCCGCGGAGATCCAGTACGCGATCGAGACAC 360
DB 318 CGTTCGACAGCGGCTTACGAGACCCGCGGTGAGGCGGAGAGAGAGCTGACCAAGCAGG 377
QY 361 CGGCAATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
DB 378 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 437
QY 421 GCTTCGTCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
DB 438 GCTGCCCATCGAGCTCGCCACCGGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 497
QY 481 CACCGCGCGCTTCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
DB 498 CACCGTCCCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 557
QY 541 CTCCCGGTCGCGGTCGTCGCG-----GCCATCGGAGCAACCGGAGCGAGCT 588
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QY 589 CTCTTACCTTCAACCGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 648
DB 618 CGGCTTCCTGCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 677
QY 649 CTCCGCGCATCGCGCTTCCAGAGCAACCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCG 708
DB 678 CGCCGAGAGCGGCTTCAAGCTCGAGAGCGAGCAACTACCGGCTGTGCTCAACCGGACCG 737

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QY 769 CGTTCCTCAACGACTGCTCTTCCGCTTCTCTCTTACGTGACCAACATCATGAGAGTGA- 827
DB 798 CGACAGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 857
QY 828 -----TGACCGCGCGGAGACCGCGGATGAGGCTTCAATCCCGGCTCCGCGTATCCCGTT 882
DB 858 CAAAGTCAACGCTTCCGCGCGCGGTTACGATGCGCTGGGTCCGCAAGAAAGTGTGCGCGC 917
QY 883 CTTCCGCGAGAGAGCGGTCGCGCGAGAGACCTTCCGCGCGCATACCGTGAACCAACCGGCG 942
DB 918 GGGCTTCGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 977
QY 943 CCGCTTCTCTTCCCGGACCTTCCGCGCGCTTCTGAGT 978
DB 978 CGGCTGTTCGTGAGAGCTTCCGCGCGCGGACCGT 1013

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